```
                    GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on:        June 29, 2004, 18:16:47 ; Search time 23 Seconds
                              (without alignments)
                       1207.599 Million cell updates/sec

Title:          US-09-892-360-2
Perfect score:  2760
Sequence:       1 MFFLYTDFFLSLVAVPAAAP.........IPTDTKDREPENNSLLEDRN 538

Scoring table:  BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched:       389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters:       389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Issued Patents AA:*
        1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
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        6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

                           SUMMARIES
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| Result No. | Score | % Match | Query Length | DB | ID | Description |
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| 1 | 1248.5 | 45.2 | 411 | 3 | US-09-236-080-6 | Sequence 6, Appli |
| 2 | 1242.5 | 45.0 | 411 | 3 | US-09-236-080-2 | Sequence 2, Appli |
| 3 | 1242.5 | 45.0 | 411 | 4 | US-09-336-643A-83 | Sequence 83, Appli |
| 4 | 1238.5 | 44.9 | 370 | 4 | US-09-144-914-8 | Sequence 8, Appli |
| 5 | 812.5 | 29.4 | 393 | 4 | US-09-432-470-2 | Sequence 2, Appli |
| 6 | 812.5 | 29.4 | 393 | 4 | US-09-432-470-4 | Sequence 4, Appli |
| 7 | 483 | 17.5 | 499 | 4 | US-09-561-763-2 | Sequence 2, Appli |
| 8 | 483 | 17.5 | 499 | 4 | US-09-431-367B-2 | Sequence 2, Appli |
| 9 | 447 | 16.2 | 107 | 3 | US-09-236-080-4 | Sequence 4, Appli |
| 10 | 403 | 14.6 | 336 | 3 | US-08-749-816-2 | Sequence 2, Appli |
| 11 | 403 | 14.6 | 336 | 4 | US-09-144-914-2 | Sequence 2, Appli |
| 12 | 396 | 14.3 | 332 | 4 | US-09-561-763-5 | Sequence 5, Appli |
| 13 | 396 | 14.3 | 332 | 4 | US-09-431-367B-5 | Sequence 5, Appli |
| 14 | 361 | 13.1 | 361 | 4 | US-09-362-842-14 | Sequence 14, Appl |
| 15 | 352.5 | 12.8 | 405 | 4 | US-09-144-914-5 | Sequence 5, Appli |
| 16 | 349.5 | 12.7 | 394 | 4 | US-09-144-914-4 | Sequence 4, Appli |
| 17 | 333.5 | 12.1 | 313 | 4 | US-09-336-643A-81 | Sequence 81, Appl |
| 18 | 333.5 | 12.1 | 313 | 4 | US-09-561-763-8 | Sequence 8, Appli |
| 19 | 333.5 | 12.1 | 313 | 4 | US-09-431-367B-8 | Sequence 8, Appli |
| 20 | 323 | 11.7 | 408 | 4 | US-09-362-842-12 | Sequence 12, Appl |
| 21 | 290.5 | 10.5 | 618 | 1 | US-08-332-312-2 | Sequence 2, Appli |
| 22 | 233.5 | 8.5 | 995 | 4 | US-09-362-842-2 | Sequence 2, Appli |
| 23 | 233 | 8.4 | 395 | 4 | US-09-362-842-6 | Sequence 6, Appli |
| 24 | 220 | 8.0 | 401 | 4 | US-09-561-763-11 | Sequence 11, Appl |
| 25 | 220 | 8.0 | 401 | 4 | US-09-431-367B-11 | Sequence 11, Appl |
| 26 | 212.5 | 7.7 | 336 | 1 | US-08-332-312-4 | Sequence 4, Appli |
| 27 | 197 | 7.1 | 730 | 4 | US-09-362-842-4 | Sequence 4, Appli |
| 28 | 197 | 7.1 | 741 | 4 | US-09-362-842-67 | Sequence 67, Appl |
| 29 | 186.5 | 6.8 | 1153 | 4 | US-09-362-842-8 | Sequence 8, Appli |
| 30 | 164.5 | 6.0 | 347 | 3 | US-08-749-816-3 | Sequence 3, Appli |
| 31 | 164.5 | 6.0 | 347 | 4 | US-09-144-914-6 | Sequence 6, Appli |
| 32 | 159 | 5.8 | 383 | 4 | US-08-749-816-4 | Sequence 4, Appli |
| 33 | 159 | 5.8 | 383 | 4 | US-09-144-914-7 | Sequence 7, Appli |
| 34 | 137.5 | 5.0 | 146 | 4 | US-09-362-842-69 | Sequence 69, Appl |
| 35 | 134 | 4.9 | 197 | 4 | US-09-336-643A-16 | Sequence 16, Appl |
| 36 | 126.5 | 4.6 | 989 | 4 | US-09-694-777A-4 | Sequence 4, Appli |
| 37 | 125 | 4.5 | 677 | 4 | US-09-177-650-4 | Sequence 4, Appli |
| 38 | 123.5 | 4.5 | 962 | 4 | US-09-614-480-9 | Sequence 9, Appli |
| 39 | 123.5 | 4.5 | 962 | 4 | US-09-694-777A-3 | Sequence 3, Appli |
| 40 | 118.5 | 4.3 | 446 | 4 | US-10-162-012-8 | Sequence 8, Appli |
| 41 | 118.5 | 4.3 | 676 | 3 | US-09-135-021-2 | Sequence 2, Appli |
| 42 | 118.5 | 4.3 | 676 | 3 | US-09-135-020-2 | Sequence 2, Appli |
| 43 | 118.5 | 4.3 | 676 | 3 | US-09-135-010A-2 | Sequence 2, Appli |
| 44 | 118.5 | 4.3 | 676 | 4 | US-09-444-871-2 | Sequence 2, Appli |
| 45 | 118.5 | 4.3 | 676 | 4 | US-09-634-920-2 | Sequence 2, Appli |

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                           ALIGNMENTS

RESULT 1
US-09-236-080-6

; Sequence 6, Application US/09236080
; Patent No. 624217
; GENERAL INFORMATION:
;   APPLICANT: Helen Meadows
;   APPLICANT: Conrad Chapman
;   TITLE OF INVENTION: No. 6242217e1 Compounds
;   FILE REFERENCE: GP30031
;   CURRENT APPLICATION NUMBER: US/09/236,080
;   CURRENT FILING DATE: 1999-01-25
;   NUMBER OF SEQ ID NOS: 6
;   SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 6
;   LENGTH: 411
;   TYPE: PRT
;   ORGANISM: Mus musculus
US-09-236-080-6

Query Match             45.2%;  Score 1248.5;  DB 3;  Length 411;
Best Local Similarity   64.3%;  Pred. No. 9.6e-107;
Matches  247;  Conservative  53;  Mismatches  67;  Indels  17;  Gaps  5;

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Qy       76 FVVVVYLVTGGLVFRALEQPFSSQKNTIALEKAEFLRDHVCVSPQELETLIQHALDAD  135
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Db       51 FLVVVLYLLIGAAVFKALEQPEISQRTTIVIQKQTFIAQHACVNSTELDELIQQIVAAI  110

Qy      136 NAGVSPIGNSSNNSSHWDLGSAFFFAGTVITTIGYGNIAPSTEGGKIFCILYAIFGIPLF  195
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Db      111 NAGIIPLGNSSNQVSHWDLGSSFFFAGTVITTIGFGNISPRTEGGKIFCIIYALLGIPLF  170

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Db      171 GFLLAGVGDQLGTIFGKGIAKVEDTFIKWNVSQTKIRIISTIIFILFGCVLFVALPAVIF  230

Qy      256 KYIEGWTALAESIYFVVVLTTVGFGDFVAGGNAGINYREWYKPLVWFWILVGLAYFAAVL  315
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Db      231 KHIEGWSALDAIYPVVILTTIGFGDYYAGG-SDIEYLDFYKPVVWFWILVGLAYFAAVL  289

Qy      316 SMIGDWLRVLSKKTKEEVGEIKAHAAEWKANVTAEFRETRRRLLSVEIHDKLQRAATIRSM  375
            ||||||||||:||||||||||:|||||||||||||||||||||||||:|| :
Db      290 SMIGDWLRVISKKTKEEVGEFRAHAAEWTANVTAEFKETRRRLLSVEIYDKFQRATSV---  346

Qy      376 ERRRLGLDQRAHSLDMLSPEKRSV  399
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Db      347 -KRKLSAELAGNHNQELITPCMRTL  369
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; Sequence 2, Application US/09236080
; Patent No. 6242217
; GENERAL INFORMATION:
; APPLICANT: Helen Meadows
; APPLICANT: Conrad Chapman
; TITLE OF INVENTION: No. 6242217el Compounds
; FILE REFERENCE: GP30031
; CURRENT APPLICATION NUMBER: US/09/236,080
; CURRENT FILING DATE: 1999-01-25
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 411
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-236-080-2

Query Match           45.0%;    Score 1242.5; DB 3;  Length 411;
Best Local Similarity 63.5%;    Pred. No. 3.4e-106;
Matches 244;  Conservative  57;  Mismatches  66;  Indels  17;  Gaps  5;

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Qy    76  FVVVVYLVTGGLVFRALEQPFESSQKNTIALEKAEFLRDHVCVSPQELETLIQHALDAD  135
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Qy   136  NAGVSPIGNSSNNSSHWDLGSAFFFAGTVITTIGYGNIAPSTEGGKIFCILYAIFGIPLF  195
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Db   171  GFLLAGVGDQLGTIFGKGIAKVEDTFIKWNVSQTKIRIISTIIFILFGCVLFVALPAIIF  230

Qy   256  KYIEGWTALESIYFVVVTLTTVGFGDFVAGGNAGINYREWYKPLVWFWILVGLAYFAAVL  315
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Db   290  SMIGDWLRVISKKTKEEVGEFRAHAAEWTANVTAEFKETRRRLSVEIYDKFQRATSI---  346

Qy   376  ERRRIGLDQRAHSLDMLSPEKRSV  399
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Db   347  -KRKLSAELAGNHNQELTPCRRTL  369

RESULT 3
US-09-336-643A-83
; Sequence 83, Application US/09336643A
; Patent No. 6399761
; GENERAL INFORMATION:
; APPLICANT: Miller, Andrew P.
; APPLICANT: Curran, Mark Edward
; APPLICANT: Hu, Ping
; APPLICANT: Rutter, Marc
; APPLICANT: Wang, Jian-Wang
; TITLE OF INVENTION: No. 6399761el Human Potassium Channels
; FILE REFERENCE: SEQ-15P
; CURRENT APPLICATION NUMBER: US/09/336,643A
; CURRENT FILING DATE:  1999-06-18
; PRIOR APPLICATION NUMBER: 60/076,687
; PRIOR APPLICATION FILING DATE: 1998-08-07
; PRIOR APPLICATION NUMBER: 60/116,448
; PRIOR APPLICATION FILING DATE: 1999-01-19
; PRIOR APPLICATION NUMBER: PCT/US99/03826
; PRIOR FILING DATE: 1999-02-22
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 83
; LENGTH: 411
; TYPE: PRT
; ORGANISM: H. sapiens
US-09-336-643A-83

Query Match           45.0%;    Score 1242.5; DB 4;  Length 411;
Best Local Similarity 63.5%;    Pred. No. 3.4e-106;
Matches 244;  Conservative  57;  Mismatches  66;  Indels  17;  Gaps  5;

Qy    17  AAAPVCQPKSATNGQPPAPAPTPTPRLSISSRATVVA-RMEGTSQGGLQTVMKWKTVVAI  75
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Qy    76  FVVVVYLVTGGLVFRALEQPFESSQKNTIALEKAEFLRDHVCVSPQELETLIQHALDAD  135
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Qy   136  NAGVSPIGNSSNNSSHWDLGSAFFFAGTVITTIGYGNIAPSTEGGKIFCILYAIFGIPLF  195
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Db   111  NAGIIPLGNTSNQISHWDLGSSFFFAGTVITTIGFGNISPRTEGGKIFCIIYALLGIPLF  170

Qy   196  GFLLAGIGDQLGTIFGKSIARVEKVFRKKQVSQTKIRVISTILFILLAGCIVFVTIPAVIF  255
              ||||||:||||||||||:|  :||..|:|||||||||::||:|||| : :|||||| ||
Db   171  GFLLAGVGDQLGTIFGKGIAKVEDTFIKWNVSQTKIRIISTIIFILFGCVLFVALPAIIF  230

Qy   256  KYIEGWTALESIYFVVVTLTTVGFGDFVAGGNAGINYREWYKPLVWFWILVGLAYFAAVL  315
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Db   231  KHIEGWSALDAIYFVVITLTTIGFGDYVAGG-SDIEYLDFYKPVVWFWILVGLAYFAAVL  289

Qy   316  SMIGDWLRVLSKKTKEEVGEIKAHAAEWKANVTAEFRETRRRLSVEIHDKLQRAATIRSM  375
              |||||||||:|||||||||| || ||:||||||||||| |::|:||||:|:|||| |:
Db   290  SMIGDWLRVISKKTKEEVGEFRAHAAEWTANVTAEFKETRRRLSVEIYDKFQRATSI---  346

Qy   376  ERRRIGLDQRAHSLDMLSPEKRSV  399
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Db   347  -KRKLSAELAGNHNQELTPCRRTL  369

RESULT 4
US-09-144-914-8
; Sequence 8, Application US/09144914
; Patent No. 6309855
; GENERAL INFORMATION:
; APPLICANT: Duprat, Fabrice
; APPLICANT: Lesage, Florian
; APPLICANT: Fink, Michel
; APPLICANT: Lazdunski, Michel
; TITLE OF INVENTION: FAMILY OF MAMMALIAN POTASSIUM CHANNELS, THEIR CLONING
; TITLE OF INVENTION: AND THEIR USE, ESPECIALLY FOR THE SCREENING OF DRUGS
; FILE REFERENCE: 989.6705CIP
; CURRENT APPLICATION NUMBER: US/09/144,914
; CURRENT FILING DATE: 1998-09-01
; EARLIER APPLICATION NUMBER: 08/749,816
; EARLIER FILING DATE: 1996-11-15
; EARLIER APPLICATION NUMBER: 60/095,234
; EARLIER FILING DATE: 1998-08-04
; EARLIER APPLICATION NUMBER: FR 96/01565
; EARLIER FILING DATE: 1996-02-08
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Murine
; FEATURE:
; OTHER INFORMATION: TREK-1
US-09-144-914-8

Query Match           44.9%;    Score 1238.5;    DB 4;  Length 370;

Best Local Similarity   64.2%;    Pred. No. 6.8e-106;
Matches  246;   Conservative   52;   Mismatches   68;   Indels   17;   Gaps    5;

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Qy    76  FVVVVYLVTGGLVFRALBQPFESSQKNTIALEKAEFLRDHVCVSPQELETLICHALDAD  135
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Db    51  FLVVVLYLIIGAAVFKALEQPQEISQRTTIVIQKQTFIAQHACVNSTELDELIQIVAAI  110

Qy   136  NAGVSPIGNSSNNSHWDLGSAFFFAGTVITTIGYGNIAPSTEGGKIFCILYAIFGIPLF  195
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Db   111  NAGIIPLGNSNQVSHWDLGSFFFAGTVITTIGFGNISPRTEGGKIFCIIYALLGIPLE  170

Qy   196  GFLLAGIGDQLGTIFGKSIARVEKVFRKKQVSQTKIRVISTILFILAGCIVFVTIPAVIF  255
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Db   171  GFLLAGVGDQLGTIFGKGIAKVEDTFIKWNVSQTKIRIISTIIFILFGCVLFVALPAVIF  230

Qy   256  KYIEGWTALESIYFVVVTLTTVGFGDFVAGGNAGINYREWKPLVWFWILVGLAYFAAVL  315
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Db   231  KHIEGWSALDAIYFVITLITTIGFGDYVAGG-SDIEYLDFYKPVVWFWILVGLAYFAAVL  289

Qy   316  SMIGDWLRVLSKKTKEEVGEIKAHAAEWKANVTAEFRETRRRLSVEIHDKLQRAATIRSM  375
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Db   290  SMIGDWLRVISKKTKEEVGEFRAHAAEWTANVTAEFKETRRRLSVEIYDKFQRATSV--  346

Qy   376  ERRRLGLDQRAHSLDMLSPEKRS  398
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Db   347  -KRKLSAELAGNHNQLTPCMRT  368
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RESULT 5
US-09-432-470-2
; Sequence 2, Application US/09432470
; Patent No. 6426197
; GENERAL INFORMATION:
; APPLICANT: David Malcolm Duckworth
; APPLICANT: Conrad Gerald Chapman
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP-30190
; CURRENT APPLICATION NUMBER: US/09/432,470
; CURRENT FILING DATE: 1999-11-03
; EARLIER APPLICATION NUMBER: UK 9923668.9
; EARLIER FILING DATE: 1999-10-07
; EARLIER APPLICATION NUMBER: UK 9824048.4
; EARLIER FILING DATE: 1998-11-03
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 393
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-432-470-2

Query Match   29.4%;   Score 812.5;   DB 4;   Length 393;
Best Local Similarity   53.8%;   Pred. No. 1.6e-66;
Matches  157;   Conservative   53;   Mismatches   77;   Indels   5;   Gaps   3;

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Qy   127  LIQHALDADNAGVSPIGNSSNNSSH--WDLGSAFFFAGTVITTIGYGNIAPSTEGGKIFC  184
              ||: |||| ::|||:|| |||||||:|:: :::|
Db    61  LIKEVADALGGGADPETNSTSNSSHSAWDLGSAFFFSGTIITTIGYGNVALRTDAGRLFC  120

Qy   185  ILYAIFGIPLFGFLLAGIGDQLGTIFGKSIARVEKVFRKKQVSQTKIRVISTILFILAGC  244
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Db   121  IFYALVGIPLFGILLAGVGDRLGSSLRHGIHIEAIFLKWHVPPELVRVLSAMLFLLIGC  180

Qy   245  IVFVTIPAVIFKYIEGWTALESIYFVVVTLTTVGFGDFVAGGNAGINYREWYKPLVWFWI  304
              ::|| ||| |:|:|||| |||||| |::: |::|||| |: |:|: :|||:||||||||
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Db   181  LLFVLTPTFVFCYMEDWSKLEAIYFVIVTLTTVGFGDYVAGADPRQD-SPAYQPLVWFWI  239

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US-09-432-470-4
; Sequence 4, Application US/09432470
; Patent No. 6426197
; GENERAL INFORMATION:
; APPLICANT: David Malcolm Duckworth
; APPLICANT: Conrad Gerald Chapman
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP-30190
; CURRENT APPLICATION NUMBER: US/09/432,470
; CURRENT FILING DATE: 1999-11-03
; EARLIER APPLICATION NUMBER: UK 9923668.9
; EARLIER FILING DATE: 1999-10-07
; EARLIER APPLICATION NUMBER: UK 9824048.4
; EARLIER FILING DATE: 1998-11-03
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 393
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-432-470-4

Query Match   29.4%;   Score 812.5;   DB 4;   Length 393;
Best Local Similarity   53.8%;   Pred. No. 1.6e-66;
Matches  157;   Conservative   53;   Mismatches   77;   Indels   5;   Gaps   3;

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Qy    67  MKWKTVVAIFVVVVVYLVTGGLVFRALEQPFESSQKNTIALEKAEFLRDHVCVSPQELET  126
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Qy   127  LIQHALDADNAGVSPIGNSSNNSSH--WDLGSAFFFAGTVITTIGYGNIAPSTEGGKIFC  184
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Db    61  LIKEVADALGGGADPETNSTSNSSHSAWDLGSAFFFSGTIITTIGYGNVALRTDAGRLFC  120

Qy   185  ILYAIFGIPLFGFLLAGIGDQLGTIFGKSIARVEKVFRKKQVSQTKIRVISTILFILAGC  244
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Db   121  IFYALVGIPLFGILLAGVGDRLGSSLRHGIHIEAIFLKWHVPPELVRVLSAMLFLLIGC  180

Qy   245  IVFVTIPAVIFKYIEGWTALESIYFVVVTLTTVGFGDFVAGGNAGINYREWYKPLVWFWI  304
              ::|| ||| |:|:|||| |||||| |::: |::|||| |: |:|: :|||:||||||||
Db   181  LLFVLTPTFVFCYMEDWSKLEAIYFVIVTLTTVGFGDYVAGADPRQD-SPAYQPLVWFWI  239

Qy   305  LVGLAYFAAVLSMIGDWLRVLSKKTKEEVGEIKAHAAEWKANVTAEFRETRR  356
              :::|||||| |:|||||||::|||||| |:||| ||: :||| |:|||:|
Db   240  LLGLAYFASVLTTIGNWLRVVSRRTRAEMGGLTAQAASWTGTVTA--RVTQR  289
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RESULT 7
US-09-561-763-2
; Sequence 2, Application US/09561763
; Patent No. 6664373
; GENERAL INFORMATION:
; APPLICANT: Curtis, Rory A.J. et al.
; TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR
; FILE REFERENCE: MNI-074CP2
; CURRENT APPLICATION NUMBER: US/09/561,763
; CURRENT FILING DATE: 2000-04-29
; PRIOR APPLICATION NUMBER: 09/431,367
; PRIOR FILING DATE: 01-11-1999
; PRIOR APPLICATION NUMBER: US 09/259,951
; PRIOR FILING DATE: 01-03-1999
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 499

; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-561-763-2

Query Match      17.5%;  Score 483;  DB 4;  Length 499;
Best Local Similarity  25.8%;  Pred. No. 6.2e-36;
Matches  131;  Conservative  81;  Mismatches  185;  Indels  110;  Gaps  14;

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Qy   79 VVVYLVTGGLVFRALEQPFESSQKNTIALEKAEFLRDHVCVSPQELETLIQHALDADNAG 138
           ::  ||  ::| ||:       |:: |     || :||
Db   12 IIFYLAIGAAIFEVLEEPHWKEAKKNYYTQKLLHLLKEFPCLGQEGLDKILEVVSDAAGQG 71

Qy  139 VSPIGNSSNNSSHWDLGSAFFFAGTVITTIGYGNIAPSTEGGKIFCILYAIFGIPLFGFL 198
           |:: |: |   ||      ||||||||||| |||||||:||||||||  |:|:|:|
Db   72 VAITGNQTFN--NWNWPNAMIFAATVITTIGYGNVAPKTPAGRLFCVFYGLFGVPL---C 126

Qy  199 LAGIGDQLGTIFGKSIARVEKVFRKKQVSQTKIRVISTILFILAGCIVFVTIPAVIFKYI 258
           :     | |:   :| || || ::|| ::|:||| |||||||   ||  |:  |:||:|
Db  127 LTWI-SALGKFFGGRAKRLGQFLTKRGVSLRKAQITCTVIFIVWGVLVHLVIPPFVFMVT 185

Qy  259 EGWTALESIYFVVVTLTTVGFGDFVAGNAGINYREWYKPLVWFWILVGLAYFAAVLSMI 318
           |||  | :| ||: ||  :||| |
Db  186 EGWNYIEGLYYSFITISTIGFGDFVAGVNPSANYHALYRYFVELWIYLGLA-------- 236

Qy  319 GDWLRVLSKKTKEEVGEIKAHAAEWKANVTAEFRETRRRLSVEIHDKLQRAATIRSMERR 378
           :|| :  : |: :        ::::
Db  237 --WLSLF--------------VNWKVS---------MFVEVHKAIK----KRRRRR 263

Qy  379 RLGLDQRAHSLDMLSPEKRSVFAALDTGRFKASSQESINNRPNNLRLK-----------GP 428
           :|   : :  | |:|  |     |:|   | ::: ::
Db  264 KESFESSPHSRKALQVKGSTASKDVNIFSFLSKKEETYNDLIKQIGKKAMKTSGGETGP 323

Qy  429 -EQLNKHGQG---------------------ASEDNIINKFGSTSRLITKRKNDLKKTLPED 468
           :  || |  |                      :::  :::
Db  324 GPGLGPQGGGLPALPPSLVPLVVYSKNRVPTLEEVSQTLRSKGHVSRSPDEEAVARAPED 383

Qy  469 VQKIYKTFRNYSLDEKKEEE--------------------TEKMCNSDNSSTAMLTDC 507
           |||||||||||:||||||                        :::
Db  384 SSPAPEVFMN-QLDRISEECEPWDAQDYHPLIFQDASITFVNTEAGLSDEETSKSSLEDN 442

Qy  508 I-------QQHAE---LENGMIPTDTK 524
           |         ||:        :::
Db  443 LAGEESPQQGAEAKAPLNMGEFPSSSE 469
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RESULT 8
US-09-431-367B-2
; Sequence 2, Application US/09431367B
; Patent No. 6670149
; GENERAL INFORMATION:
; APPLICANT: Curtis, Rory A.J.
; TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR
; FILE REFERENCE: MNI-074CP
; CURRENT APPLICATION NUMBER: US/09/431,367B
; CURRENT FILING DATE: 1999-11-01
; PRIOR APPLICATION NUMBER: 09/259,951
; PRIOR FILING DATE: 1999-03-01
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 499;
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-431-367B-2

Query Match      17.5%;  Score 483;  DB 4;  Length 499;
Best Local Similarity  25.8%;  Pred. No. 6.2e-36;
Matches  131;  Conservative  81;  Mismatches  185;  Indels  110;  Gaps  14;

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Qy   79 VVVYLVTGGLVFRALEQPFESSQKNTIALEKAEFLRDHVCVSPQELETLIQHALDADNAG 138
           ::  ||  ::| ||:       |:: |     || :||
Db   12 IIFYLAIGAAIFEVLEEPHWKEAKKNYYTQKLLHLLKEFPCLGQEGLDKILEVVSDAAGQG 71
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---

; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-236-080-4

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Qy  139 VSPIGNSSNNSSHWDLGSAFFFAGTVITTIGYGNIAPSTEGGKIFCILYAIFGIPLFGFL 198
           |:: |: |   ||      ||||||||||| |||||||:||||||||  |:|:|:|
Db   72 VAITGNQTFN--NWNWPNAMIFAATVITTIGYGNVAPKTPAGRLFCVFYGLFGVPL---C 126

Qy  199 LAGIGDQLGTIFGKSIARVEKVFRKKQVSQTKIRVISTILFILAGCIVFVTIPAVIFKYI 258
           :     | |:   :| || || ::|| ::|:||| |||||||   ||  |:  |:||:|
Db  127 LTWI-SALGKFFGGRAKRLGQFLTKRGVSLRKAQITCTVIFIVWGVLVHLVIPPFVFMVT 185

Qy  259 EGWTALESIYFVVVTLTTVGFGDFVAGNAGINYREWYKPLVWFWILVGLAYFAAVLSMI 318
           |||  | :| ||: ||  :||| |
Db  186 EGWNYIEGLYYSFITISTIGFGDFVAGVNPSANYHALYRYFVELWIYLGLA-------- 236

Qy  319 GDWLRVLSKKTKEEVGEIKAHAAEWKANVTAEFRETRRRLSVEIHDKLQRAATIRSMERR 378
           :|| :  : |: :        ::::
Db  237 --WLSLF--------------VNWKVS---------MFVEVHKAIK----KRRRRR 263

Qy  379 RLGLDQRAHSLDMLSPEKRSVFAALDTGRFKASSQESINNRPNNLRLK-----------GP 428
           :|   : :  | |:|  |     |:|   | ::: ::
Db  264 KESFESSPHSRKALQVKGSTASKDVNIFSFLSKKEETYNDLIKQIGKKAMKTSGGETGP 323

Qy  429 -EQLNKHGQG---------------------ASEDNIINKFGSTSRLITKRKNDLKKTLPED 468
           :  || |  |                      :::  :::
Db  324 GPGLGPQGGGLPALPPSLVPLVVYSKNRVPTLEEVSQTLRSKGHVSRSPDEEAVARAPED 383

Qy  469 VQKIYKTFRNYSLDEKKEE---------------------TEKMCNSDNSSTAMLTDC 507
           |||||||||||:|||||                         :::
Db  384 SSPAPEVFMN-QLDRISEECEPWDAQDYHPLIFQDASITFVNTEAGLSDEETSKSSLEDN 442

Qy  508 I-------QQHAE---LENGMIPTDTK 524
           |         ||:        :::
Db  443 LAGEESPQQGAEAKAPLNMGEFPSSSE 469
```

RESULT 9
US-09-236-080-4
; Sequence 4, Application US/09236080
; Patent No. 6242217
; GENERAL INFORMATION:
; APPLICANT: Helen Meadows
; APPLICANT: Conrad Chapman
; TITLE OF INVENTION: No. 6242217el Compounds
; FILE REFERENCE: GP30031
; CURRENT APPLICATION NUMBER: US/09/236,080
; CURRENT FILING DATE: 1999-01-25
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-236-080-4

Query Match      16.2%;  Score 447;  DB 3;  Length 107;
Best Local Similarity  77.6%;  Pred. No. 1.2e-33;
Matches  83;  Conservative  12;  Mismatches  12;  Indels  0;  Gaps  0;

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Qy  144 NSSNNSSHWDLGSAFFFAGTVITTIGYGNIAPSTEGGKIFCILYAIFGIPLFGFLLAGIG 203
           |:||  :||||||| |||||||||||||||||||| ||||||||||:|||||||||||||
Db    1 NSSNQVSHWDLGSSFFFAGTVITTIGFGNISPRTEGGKIFCIIYALLGIPLFGFLLAGVG 60

Qy  204 DQLGTIFGKSIARVEKVFRKKQVSQTKIRVISTILFILAGCIVFVTI 250
           |||||||||| |||| :|:  |||:|||:|| ||||||||  |:|:|
Db   61 DQLGTIFGKGIAKVEDTFIKWNVSQTKIRIISTIFIFILFGCVLFVAL 107
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RESULT 10
US-08-749-816-2
; Sequence 2, Application US/08749816
; Patent No. 601347O
; GENERAL INFORMATION:
; APPLICANT: Lesage, Florian
; APPLICANT: Guillemare, Eric
; APPLICANT: Fink, Michel

; APPLICANT: Duprat, Fabrice
; APPLICANT: Lazdunki, Michel
; APPLICANT: Romey, Georges
; APPLICANT: Barhanin, Jacques
; TITLE OF INVENTION: FAMILY OF MAMMALIAN POTASSIUM CHANNELS,
; TITLE OF INVENTION: THEIR CLONING AND THEIR USE ESPECIALLY FOR THE SCREENING
; TITLE OF INVENTION: OF DRUGS
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WEISER & ASSOCIATES
; STREET: 230 South Fifteenth Street, Suite 500
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/749,816
; FILING DATE: 15-NOV-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Weiser, Gerard J.
; REGISTRATION NUMBER: 19,763
; REFERENCE/DOCKET NUMBER: 989.6351P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-875-8383
; TELEFAX: 215-875-8394
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 336 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-749-816-2

Query Match       14.6%;   Score 403;  DB 3;  Length 336;
Best Local Similarity 33.2%;  Pred. No. 8.2e-29;
Matches   95;  Conservative  53;  Mismatches 104;  Indels 34;  Gaps 9;

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Qy   76 FVVV--VVYLVTGGLVFRALEQPFESSQKNTIALEKAEFLRDHVCVSPQELETLIQHALD 133
           |:|:  ::||||:  :||||| :| ::|:|  |:|:   || |:|:| :||  ::|
Db   25 FLVLGYLYLYLVFGAVVFSSVELPYEDLLRQELRLKLKRRFLEEHECLSEQQLEQFLGRVLE 84

Qy  134 ADNAGVSPIGNSSNNSSHWDLGSAPFFAGTVITTIGYGNIAPSTEGGKIFCILYAIFGIP 193
           |:|: ::|||:  :|| |: |:||: | :||: |:|| |||:||| :|:||:|:|:|
Db   85 ASNYGVSVLSNASGN-WNWDFTSALFFASTVLSTTGYGHTVPLSDGGKAFCIIYSVIGIP 143

Qy  194 LFGFLLAGIGDQLGTIFGKSIARVEKVFRKKQV-------SQTKIRVISTIL--FILA 242
           :| ||: | :: |   ::  :: |::    ||
Db  144 FTLLFLTAV--------VQRITVHVTRRPVLYFHIRWGFSKQVVAIVHAVLLGFVTV 192

Qy  243 GCIVFVTIPAVIFKYIE-GWTALESIYFVVVTLTTVGFGDFVAGGNAGINYREWYKPLVW 301
           |||:  :|    :|:  ::|: :|||  :|||: || ::|| ||
Db  193 SCFFF--IPAAVFSVLEDDWNFLESFYFCFISLSTIGLGDYVPGEGYNQKFRELYKIGIT 250

Qy  302 FWILVGLAYFAAVLSMIGDWLRVLSK----KTKEEVGEIKAHAAE 342
           :|:||  | ||: || :||: :|:  ||:|  ::||||
Db  251 CYLLLGLIAMLVVLETFCE-LHELKFKRKMFYVKDKDEDQVHIIE 295
```

RESULT 11
US-09-144-914-2
; Sequence 2, Application US/09144914
; Patent No. 6309855
; GENERAL INFORMATION:
; APPLICANT: Duprat, Fabrice
; APPLICANT: Lesage, Florian
; APPLICANT: Fink, Michel
; APPLICANT: Lazdunski, Michel

---

; TITLE OF INVENTION: FAMILY OF MAMMALIAN POTASSIUM CHANNELS, THEIR CLONING
; TITLE OF INVENTION: AND THEIR USE, ESPECIALLY FOR THE SCREENING OF DRUGS
; FILE REFERENCE: 989.6705CIP
; CURRENT APPLICATION NUMBER: US/09/144,914
; CURRENT FILING DATE: 1998-09-01
; EARLIER APPLICATION NUMBER: 08/749,816
; EARLIER FILING DATE: 1996-11-15
; EARLIER APPLICATION NUMBER: 60/095,234
; EARLIER FILING DATE: 1998-08-04
; EARLIER APPLICATION NUMBER: FR 96/01565
; EARLIER FILING DATE: 1996-02-08
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 336
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: TWIK-1
US-09-144-914-2

Query Match       14.6%;   Score 403;  DB 4;  Length 336;
Best Local Similarity 33.2%;  Pred. No. 8.2e-29;
Matches   95;  Conservative  53;  Mismatches 104;  Indels 34;  Gaps 9;

```
Qy   76 FVVV--VVYLVTGGLVFRALEQPFESSQKNTIALEKAEFLRDHVCVSPQELETLIQHALD 133
           |:|:  ::||||:  :||||| :| ::|:|  |:|:   || |:|:| :||  ::|
Db   25 FLVLGYLYLYLVFGAVVFSSVELPYEDLLRQELRLKLKRRFLEEHECLSEQQLEQFLGRVLE 84

Qy  134 ADNAGVSPIGNSSNNSSHWDLGSAPFFAGTVITTIGYGNIAPSTEGGKIFCILYAIFGIP 193
           |:|: ::|||:  :|| |: |:||: | :||: |:|| |||:||| :|:||:|:|:|
Db   85 ASNYGVSVLSNASGN-WNWDFTSALFFASTVLSTTGYGHTVPLSDGGKAFCIIYSVIGIP 143

Qy  194 LFGFLLAGIGDQLGTIFGKSIARVEKVFRKKQV-------SQTKIRVISTIL--FILA 242
           :| ||: | :: |   ::  :: |::    ||
Db  144 FTLLFLTAV--------VQRITVHVTRRPVLYFHIRWGFSKQVVAIVHAVLLGFVTV 192

Qy  243 GCIVFVTIPAVIFKYIE-GWTALESIYFVVVTLTTVGFGDFVAGGNAGINYREWYKPLVW 301
           |||:  :|    :|:  ::|: :|||  :|||: || ::|| ||
Db  193 SCFFF--IPAAVFSVLEDDWNFLESFYFCFISLSTIGLGDYVPGEGYNQKFRELYKIGIT 250

Qy  302 FWILVGLAYFAAVLSMIGDWLRVLSK----KTKEEVGEIKAHAAE 342
           :|:||  | ||: || :||: :|:  ||:|  ::||||
Db  251 CYLLLGLIAMLVVLETFCE-LHELKFKRKMFYVKDKDEDQVHIIE 295
```

RESULT 12
US-09-561-763-5
; Sequence 5, Application US/09561763
; Patent No. 6664373
; GENERAL INFORMATION:
; APPLICANT: Curtis, Rory A.J. et al.
; TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR
; FILE REFERENCE: MNI-074CP2
; CURRENT APPLICATION NUMBER: US/09/561,763
; CURRENT FILING DATE: 2000-04-29
; PRIOR APPLICATION NUMBER: 09/431,367
; PRIOR FILING DATE: 01-11-1999
; PRIOR APPLICATION NUMBER: US 09/255,951
; PRIOR FILING DATE: 01-03-1999
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 332
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-561-763-5

Query Match       14.3%;   Score 396;  DB 4;  Length 332;
Best Local Similarity 31.6%;  Pred. No. 3.6e-28;
Matches   86;  Conservative  58;  Mismatches 114;  Indels 14;  Gaps 3;

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Qy   47 SRATVVARMEGTSQGGLQTVMKWKITVAIFVVVVYLVTGGLVFRALEQPFESSQKNTIA 106
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;   FILE REFERENCE: 7326-104
;   CURRENT APPLICATION NUMBER: US/09/362,842
;   CURRENT FILING DATE: 1999-07-28
;   PRIOR APPLICATION NUMBER: 09/270,767
;   PRIOR FILING DATE: 1999-03-17
;   NUMBER OF SEQ ID NOS: 70
;   SOFTWARE: PatentIn Ver. 2.1
;   SEQ ID NO 14
;   LENGTH: 361
;   TYPE: PRT
;   ORGANISM: Leptinotarsa decemlineata
US-09-362-842-14

Query Match           13.1%;  Score 361;  DB 4;  Length 361;
Best Local Similarity 29.1%;  Pred. No. 6.9e-25;
Matches   86;  Conservative  62;  Mismatches 104;  Indels  44;  Gaps   7;

Qy  41 PRLSISSRATVVARMEGTSQGGLQTVMKWKTVAIFVVVVYLVTGGLVFRALEQPFESS 100
Db  26 PKIVEGNRNKIIG-MEKTS--------FRFSLYLF-AYFMFLCSGAAVFSYFEAPEERA 74
Qy 101 QKNTIALEKAEFLRDHVCVSPQELETLIQHALDADNAGVSPIGNSSNNSSHWDLGSAFFF 160
Db  75 LRVKLGTAVQKFLVSNPNVTDADLEELIVEIVRANNRGVSAIENAT-SEPNWSFGQSFFF 133
Qy 161 AGTVITTIGYGNIAPSTEGGKIFCILYAIFGIPLFGFLLAG-------IGDQ 205
Db 134 ASTVITTIGYGHVTPLSRNGKLFCMFYAVVGIPLTIVLLSALVERLLIPTWLLQWLNSK 193
Qy 206 LGTIFGKSIARVEKVFRKKQVSQTKIRVISTILFLAGGIVFVTIPAVIFKYIE-GWTAL 264
Db 194 LGHLY-----------------QPLRIRIVHLAIIVLLVLLVFFLLLPAAIFASLEPEWDYL 237
Qy 265 ESIYFVVLTTVGFDFVAGGNAGINYREWYKPLVWFWILVGLAYFAAVLSMIGD 320
Db 238 DSLYICFISLTTIGLGDYIPGDSAHQPYRPLYKIMTTCYLFLGITIMMLTLTVFYD 293


RESULT 15
US-09-144-914-5
; Sequence 5, Application US/09144914
; Patent No. 6309855
; GENERAL INFORMATION:
;   APPLICANT: Duprat, Fabrice
;   APPLICANT: Lesage, Florian
;   APPLICANT: Fink, Michel
;   APPLICANT: Lazdunski, Michel
;   TITLE OF INVENTION: FAMILY OF MAMMALIAN POTASSIUM CHANNELS, THEIR CLONING
;   TITLE OF INVENTION: AND THEIR USE, ESPECIALLY FOR THE SCREENING OF DRUGS
;   FILE REFERENCE: 989.6705CIP
;   CURRENT APPLICATION NUMBER: US/09/144,914
;   CURRENT FILING DATE: 1998-09-01
;   EARLIER APPLICATION NUMBER: 08/749,816
;   EARLIER FILING DATE: 1996-11-15
;   EARLIER APPLICATION NUMBER: 60/095,234
;   EARLIER FILING DATE: 1998-08-04
;   EARLIER APPLICATION NUMBER: FR 96/01565
;   EARLIER FILING DATE: 1996-02-08
;   NUMBER OF SEQ ID NOS: 24
;   SOFTWARE: PatentIn Ver. 2.0
;   SEQ ID NO 5
;   LENGTH: 405
;   TYPE: PRT
;   ORGANISM: Murine
;   FEATURE:
;   OTHER INFORMATION: TASK
US-09-144-914-5

Query Match           12.8%;  Score 352.5;  DB 4;  Length 405;
Best Local Similarity 32.1%;  Pred. No. 5.1e-24;
Matches   90;  Conservative  53;  Mismatches 110;  Indels 110;  Gaps   8;

Qy  73 VAIFVVVVYLVTGGLVFRALEQPFESSQKNTIALEKAEFLRDHVCVSP---QELETLIQ 129
```

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Db     ARAAPEGRVRGCAVPG--------TVLLLAYLAYLALGTGVFWTLEGRAAQDSRSRSFQ 56
Db   6 ARAAPEGRVRGCAVPG--------TVLLLAYLAYLALGTGVFWTLEGRAAQDSRSRSFQ 56
Qy 107 LEKAEFLRDHVCVSPQELETLIQHALDADNAGVSPIGNSSNNSSHWDLGSAFFFAGTVIT 166
Db  57 RDKWELLQNFTCLDRPALDSLIRDVVQAYKNGASLLSNTT-SMGRWELVGSFFSVSTIT 115
Qy 167 TIGYGNIAPSTEGGKIFCILYAIFGIPLFGFLLAGIGDQLGTIFGKSIARVEKVFRKKQV 226
Db 116 TIGYGNLSPNTMAARLFCIFFALVGIPLNLVVL----NRLGHLMQQGVNHWASRLGGTWQ 171
Qy 227 SQTKIRVISTILFLAGCIVFVTIPAVIFKYIEGWTALESIYFVVVTLTTVGFDFVAGG 286
Db 172 DPDKARWLAGSGALLSGLLLFLLLPPLLFSHMEGWSYTEGFYPAFITLSTVGFGDYVIGM 231
Qy 287 NAGINYREWYKPLVWFWILVGLAYFAAVLSMI 318
Db 232 NPSQRYPLWYKNMVSLWILFGMAWLALIIKLI 263


RESULT 13
US-09-431-367B-5
; Sequence 5, Application US/09431367B
; Patent No. 6670149
; GENERAL INFORMATION:
;   APPLICANT: Curtis, Rory A.J.
;   TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR
;   FILE REFERENCE: MNI-074CP
;   CURRENT APPLICATION NUMBER: US/09/431,367B
;   CURRENT FILING DATE: 1999-11-01
;   PRIOR APPLICATION NUMBER: 09/259,951
;   PRIOR FILING DATE: 1999-03-01
;   NUMBER OF SEQ ID NOS: 12
;   SOFTWARE: PatentIn Ver. 2.0
;   SEQ ID NO 5
;   LENGTH: 332
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-431-367B-5

Query Match           14.3%;  Score 396;  DB 4;  Length 332;
Best Local Similarity 31.6%;  Pred. No. 3.6e-28;
Matches   86;  Conservative  58;  Mismatches 114;  Indels  14;  Gaps   3;

Qy  47 SRATVVARMEGTSQGGLQTVMKWKTVAIFVVVVYLVTGGLVFRALEQPFESSQKNTIA 106
Db   6 ARAAPEGRVRGCAVPG--------TVLLLAYLAYLALGTGVFWTLEGRAAQDSRSRSFQ 56
Qy 107 LEKAEFLRDHVCVSPQELETLIQHALDADNAGVSPIGNSSNNSSHWDLGSAFFFAGTVIT 166
Db  57 RDKWELLQNFTCLDRPALDSLIRDVVQAYKNGASLLSNTT-SMGRWELVGSFFSVSTIT 115
Qy 167 TIGYGNIAPSTEGGKIFCILYAIFGIPLFGFLLAGIGDQLGTIFGKSIARVEKVFRKKQV 226
Db 116 TIGYGNLSPNTMAARLFCIFFALVGIPLNLVVL---NRLGHLMQQGVNHWASRLGGTWQ 171
Qy 227 SQTKIRVISTILFLAGCIVFVTIPAVIFKYIEGWTALESIYFVVVTLTTVGFDFVAGG 286
Db 172 DPDKARWLAGSGALLSGLLLFLLLPPLLFSHMEGWSYTEGFYPAFITLSTVGFGDYVIGM 231
Qy 287 NAGINYREWYKPLVWFWILVGLAYFAAVLSMI 318
Db 232 NPSQRYPLWYKNMVSLWILFGMAWLALIIKLI 263


RESULT 14
US-09-362-842-14
; Sequence 14, Application US/09362842
; Patent No. 6511824
; GENERAL INFORMATION:
;   APPLICANT: Buchman et al.
;   TITLE OF INVENTION: NUCLEIC ACIDS AND POLYPEPTIDES OF INVERTEBRATE TWIK
;   TITLE OF INVENTION: CHANNELS AND METHODS OF USE
```

```
          :|:.|      .||:.|   || ||||             :|  .:||        :|||.:|:
Db     6  LALIVCTFTYLLVGAAVFDALESEPEMIERQRLELRQLE-LRARYNLSEGGYEELERVVL  64

              .||                   :.|:|| ||||||||:|||:||:.||:.||:
Qy   130  HALDADNAGVSPIGNSSNNSSHWDLGSAFFPAGTVITTIGYGNIAPSTEGKIFCILYAI  189
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Qy   190  FGIPLFGFLLAGIGDQLGTIFGKSIARVEKVFRKKQVSQTKIRVISTILFILAGCIVFVT  249
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Db   170  IGAAAFSYYERWTFFQAYYYCFITLTTIGFGDYVALQKDQALQTQPQYVAFSFVYILTGL  229

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Search completed: June 29, 2004, 18:20:32
Job time : 24 secs

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                    GenCore version 5.1.6

         Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on:      June 29, 2004, 18:19:28 ; Search time 50 Seconds
                                        (without alignments)
                                        3041.909 Million cell updates/sec

Title:       US-09-892-360-2
Perfect score: 2760
Sequence:    1 MFFLYTDFFLSLVAVPAAAP.........IPTDTKDREPENNSLLEDRN 538

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched:    1166195 seqs, 282705291 residues

Total number of hits satisfying chosen parameters:      1166195

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB | ID | Description |
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| 1 | 2760 | 100.0 | 538 | 12 | US-09-892-360-2 | Sequence 2, Appli |
| 2 | 2697 | 97.7 | 526 | 9 | US-09-729-920-4 | Sequence 4, Appli |
| 3 | 2697 | 97.7 | 543 | 9 | US-09-729-920-2 | Sequence 2, Appli |
| 4 | 2697 | 97.7 | 543 | 12 | US-10-262-511-106 | Sequence 106, App |
| 5 | 2697 | 97.7 | 543 | 12 | US-09-852-386-73 | Sequence 73, Appl |
| 6 | 2697 | 97.7 | 543 | 14 | US-10-332-175-2 | Sequence 2, Appli |
| 7 | 2657.5 | 96.3 | 724 | 12 | US-10-332-447-10 | Sequence 10, Appl |
| 8 | 2560.5 | 92.8 | 538 | 9 | US-09-729-920-5 | Sequence 5, Appli |
| 9 | 1248.5 | 45.2 | 411 | 9 | US-09-828-746-6 | Sequence 6, Appli |
| 10 | 1243 | 45.0 | 411 | 12 | US-09-892-360-18 | Sequence 18, Appl |
| 11 | 1242.5 | 45.0 | 411 | 9 | US-09-828-746-2 | Sequence 2, Appli |
| 12 | 1242.5 | 45.0 | 411 | 14 | US-10-121-746-83 | Sequence 83, Appl |
| 13 | 1238.5 | 44.9 | 370 | 9 | US-09-939-484-8 | Sequence 8, Appli |
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| 15 | 1218.5 | 44.1 | 426 | 8 | US-08-816-011-45 | Sequence 45, Appl |

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| 16 | 825.5 | 29.9 | 1314 | 9 | US-09-747-835A-29 | Sequence 29, Appl |
| 17 | 825.5 | 29.9 | 1314 | 12 | US-10-312-312-29 | Sequence 29, Appl |
| 18 | 822.5 | 29.8 | 419 | 9 | US-09-828-035-2 | Sequence 2, Appli |
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| 20 | 822.5 | 29.8 | 419 | 14 | US-10-146-733-29 | Sequence 29, Appl |
| 21 | 822.5 | 29.8 | 419 | 15 | US-10-352-684A-8 | Sequence 8, Appli |
| 22 | 822.5 | 29.8 | 419 | 15 | US-10-391-399-19 | Sequence 19, Appl |
| 23 | 812.5 | 29.4 | 392 | 9 | US-09-747-835A-55 | Sequence 55, Appl |
| 24 | 812.5 | 29.4 | 392 | 12 | US-10-312-312-55 | Sequence 55, Appl |
| 25 | 812.5 | 29.4 | 393 | 14 | US-10-243-035-2 | Sequence 2, Appli |
| 26 | 790 | 28.6 | 398 | 12 | US-09-892-360-19 | Sequence 19, Appl |
| 27 | 610.5 | 22.1 | 421 | 12 | US-10-276-774-2599 | Sequence 2599, Ap |
| 28 | 512 | 18.6 | 294 | 12 | US-10-451-892-2 | Sequence 2, Appli |
| 29 | 512 | 18.6 | 294 | 12 | US-10-459-190-2 | Sequence 9, Appli |
| 30 | 512 | 18.6 | 294 | 12 | US-10-459-190-9 | Sequence 2, Appli |
| 31 | 512 | 18.6 | 294 | 13 | US-10-121-966-2 | Sequence 172, App |
| 32 | 512 | 18.6 | 309 | 15 | US-10-080-334-172 | Sequence 177, App |
| 33 | 512 | 18.6 | 309 | 15 | US-10-080-334-177 | Sequence 11, Appl |
| 34 | 511 | 18.5 | 239 | 12 | US-10-459-190-11 | Sequence 6, Appli |
| 35 | 511 | 18.5 | 292 | 12 | US-10-451-892-6 | Sequence 10, Appl |
| 36 | 511 | 18.5 | 292 | 12 | US-10-451-892-10 | Sequence 4, Appli |
| 37 | 511 | 18.5 | 292 | 12 | US-10-459-190-4 | Sequence 2, Appli |
| 38 | 483 | 17.5 | 499 | 9 | US-09-735-169A-2 | Sequence 2, Appli |
| 39 | 483 | 17.5 | 499 | 9 | US-09-735-171A-2 | Sequence 2, Appli |
| 40 | 483 | 17.5 | 499 | 12 | US-10-701-013-2 | Sequence 10, Appl |
| 41 | 478 | 17.3 | 294 | 12 | US-10-459-190-10 | Sequence 13, Appl |
| 42 | 455 | 16.5 | 239 | 12 | US-10-459-190-13 | Sequence 4, Appli |
| 43 | 447 | 16.2 | 107 | 9 | US-09-828-746-4 | Sequence 2, Appli |
| 44 | 403 | 14.6 | 336 | 9 | US-09-939-484-2 | Sequence 2, Appli |
| 45 | 403 | 14.6 | 336 | 9 | US-09-939-483-2 | |

ALIGNMENTS

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RESULT 1
US-09-892-360-2
; Sequence 2, Application US/09892360
; Publication No. US2004010101833A1
; GENERAL INFORMATION:
;  APPLICANT: LAZDUNSKI, MICHEL
;  APPLICANT: LESAGE, FLORIAN
;  APPLICANT: ROMEY, GEORGES
;  TITLE OF INVENTION: HUMAN TREK2, A STRETCH-AND ARACHIDONIC ACID-SENSITIVE
;  TITLE OF INVENTION:  K+ CHANNEL ACTIVATED BY INHALATIONAL ANESTHETICS AND
;  TITLE OF INVENTION: RILUZOLE
;  FILE REFERENCE: 1256-R-00
;  CURRENT APPLICATION NUMBER: US/09/892,360
;  CURRENT FILING DATE:  2001-06-27
;  PRIOR APPLICATION NUMBER: 60/214,559
;  PRIOR FILING DATE: 2000-06-27
;  NUMBER OF SEQ ID NOS: 25
;  SOFTWARE: PatentIn Ver. 2.1
;
; SEQ ID NO 2
;  LENGTH: 538
;  TYPE: PRT
;  ORGANISM: Homo sapiens
US-09-892-360-2

Query Match             100.0%;  Score 2760;  DB 12;  Length 538;
Best Local Similarity   100.0%;  Pred. No. 8.2e-230;
Matches  538;   Conservative    0;   Mismatches    0;   Indels    0;   Gaps    0;

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Qy     61 GGLQTVMKWKTVVAIFVVVVYLVTGGLVFRALEQPFESSQKNTIALEKAEFLRDHVCVS 120
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Db     61 GGLQTVMKWKTVVAIFVVVVYLVTGGLVFRALEQPFESSQKNTIALEKAEFLRDHVCVS 120

Qy    121 PQELETLIQHALDADNAGVSPIGNSSNNSSHWDLGSAFFAGTVITTIGYGNIAPSTEGG 180
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Db  121 PQELETLIQHALDADNAGVSPIGNSSNNSSHWDLGSAFFFAGTVITTIGYGNIAPSTEGG 180

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Qy  301 WFWILVGLAYFAAVLSMIGDWLRVLSKKTKEEVGEIKAHAAEWKANVTAEFRETRRRLSV 360
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Qy  361 EIHDKLQRAATIRSMERRRLGLDQRAHSLDMLSPEKRSVFAALDTGRFKASSQESINNRP 420
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RESULT 2
US-09-729-920-4
; Sequence 4, Application US/09729920
; Patent No. US2002010311SA1
; GENERAL INFORMATION:
; APPLICANT: GUGLER, Karl et al
; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CL000858
; CURRENT APPLICATION NUMBER: US/09/729,920
; CURRENT FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 526
; TYPE: PRT
; ORGANISM: Human
US-09-729-920-4

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Query Match            97.7%;  Score 2697;  DB 9;  Length 526;
Best Local Similarity 100.0%;  Pred. No. 2.2e-224;
Matches 526;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

Qy   13 VAVPAAAPVCQPKSATNGQPPAPAPTPTPRLSISSRATVVARMEGTSQGGLQTVMKWKTV 72
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Db    1 VAVPAAAPVCQPKSATNGQPPAPAPTPTPRLSISSRATVVARMEGTSQGGLQTVMKWKTV 60

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Db  121 DADNAGVSPIGNSSNNSSHWDLGSAFFFAGTVITTIGYGNIAPSTEGGKIFCILYAIFGI 180

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Db  181 PLFGFLLAGIGDQLGTIFGKSIARVEKVFRKKQVSQTKIRVISTILFILAGCIVFVTIPA 240

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; Sequence 2, Application US/09729920
; Patent No. US2002010311SA1
; GENERAL INFORMATION:
; APPLICANT: GUGLER, Karl et al
; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CL000858
; CURRENT APPLICATION NUMBER: US/09/729,920
; CURRENT FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 543
; TYPE: PRT
; ORGANISM: Human
US-09-729-920-2

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Query Match            97.7%;  Score 2697;  DB 9;  Length 543;
Best Local Similarity 100.0%;  Pred. No. 2.3e-224;
Matches 526;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

Qy   13 VAVPAAAPVCQPKSATNGQPPAPAPTPTPRLSISSRATVVARMEGTSQGGLQTVMKWKTV 72
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Db  138 DADNAGVSPIGNSSNNSSHWDLGSAFFFAGTVITTIGYGNIAPSTEGGKIFCILYAIFGI 197

Qy  193 PLFGFLLAGIGDQLGTIFGKSIARVEKVFRKKQVSQTKIRVISTILFILAGCIVFVTIPA 252
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Db  258 VIFKYIEGWTALESIYFVVVTLTTVGFGDFVAGGNAGINYREWYKPLVWFWILVGLAYFA 317

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Db  438 KHGQGASEDNIINKFGSTSRLTKRKNKDLKKTLPEDVQKIYKTFRNYSLDEEKKEETEK 497

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Qy    73 VAIFVVVVVLVTGGLVFRALEQPFESSQKNTIALEKAEFLRDHVCVSPQELETLIQHAL 132
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Db   138 DADNAGVSPIGNSSNNSSHWDLGSAFFFAGTVITTIGYGNIAPSTEGGKIFCILYAIFGI 197

Qy   193 PLFGFLLAGIGDQLGTIFGKSIARVEKVFRKKQVSQTKIRVISTILFILAGCIVFVTIPA 252
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   198 PLFGFLLAGIGDQLGTIFGKSIARVEKVFRKKQVSQTKIRVISTILFILAGCIVFVTIPA 257

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             ||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db   318 AVLSMIGDWLRVLSKKTKEEVGEIKAHAAEWKANVTAEFRETRRLSVEIHDKLQRAATI 377

Qy   373 RSMERRRLGLDQRAHSLDMLSPEKRSVFAALDTGRFKASSQESINNRPNNLRLKGPEQLN 432
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   378 RSMERRRLGLDQRAHSLDMLSPEKRSVFAALDTGRFKASSQESINNRPNNLRLKGPEQLN 437

Qy   433 KHGQGASEDNIINKFGSTSRLTKRKNKDLKKTLPEDVQKIYKTFRNYSLDEBKKEETEK 492
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Db   438 KHGQGASEDNIINKFGSTSRLTKRKNKDLKKTLPEDVQKIYKTFRNYSLDEBKKEETEK 497

Qy   493 MCNSDNSSTAMLTDCIQQHAELENGMIPTDTKDREPENNSLLEDRN 538
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Db   498 MCNSDNSSTAMLTDCIQQHAELENGMIPTDTKDREPENNSLLEDRN 543
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RESULT 4
US-10-262-511-106
; Sequence 106, Application US/10262511
; Publication No. US20040003823A1
; GENERAL INFORMATION:
; APPLICANT: Smithson, Glennda
; APPLICANT: Millet, Isabelle
; APPLICANT: Peyman, John A.
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Ju, Jingfang
; APPLICANT: Li, Li
; APPLICANT: Guo, Xiaojia (Sasha)
; APPLICANT: Patturajan, Meera
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Ellerman, Karen
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Ort, Tatiana
; APPLICANT: Gorman, Linda
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Anderson, David W.
; APPLICANT: Zhong, Mei
; APPLICANT: Catterton, Elina
; APPLICANT: Ji, Weizhen
; APPLICANT: Miller, Charles E.
; APPLICANT: Rastelli, Luca
; APPLICANT: Stone, David J.
; APPLICANT: Pena, Carol E. A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Rothenberg, Mark E.
; APPLICANT: Leach, Martin D.
; APPLICANT: Agee, Michele L.
; APPLICANT: Berghs, Constance
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-452C
; CURRENT APPLICATION NUMBER: US/10/262,511
; CURRENT FILING DATE: 2003-05-28
; PRIOR APPLICATION NUMBER: 60/326,483
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: 60/373,815
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/327,917
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/381,642
; PRIOR FILING DATE: 2002-05-17
; PRIOR APPLICATION NUMBER: 60/328,029
; PRIOR FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: 60/381,038
; PRIOR FILING DATE: 2002-05-16
; PRIOR APPLICATION NUMBER: 60/328,056
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/373,260
; PRIOR FILING DATE: 2002-04-17
; PRIOR APPLICATION NUMBER: 60/373,826
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/327,435
; PRIOR FILING DATE: 2001-10-05
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 439
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 106
; LENGTH: 543
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-262-511-106

Query Match          97.7%; Score 2697; DB 12; Length 543;
Best Local Similarity 100.0%; Pred. No. 2.3e-224;
Matches 526; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 5
US-09-852-386-73
; Sequence 73, Application US/09852386
; Publication No. US20030064433A1
; GENERAL INFORMATION:
; APPLICANT: Roberds, Steven L.
; APPLICANT: Benjamin, Christopher
; APPLICANT: Karnovsky, Alla M.
; APPLICANT: Ruble, Cara L.
; TITLE OF INVENTION: Human Ion Channels
; FILE REFERENCE: 00133.US1
; CURRENT APPLICATION NUMBER: US/09/852,386
; CURRENT FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: 60/203,305
; PRIOR FILING DATE: 2000-05-10
; PRIOR APPLICATION NUMBER: 60/207,092
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/206,526
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,033
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/207,093
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/216,893
; PRIOR FILING DATE: 2000-07-17
; PRIOR APPLICATION NUMBER: 60/237,873
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: 60/223,245
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 88
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 73
; LENGTH: 543
; TYPE: PRT
; ORGANISM: Homo sapiens

US-09-852-386-73

Query Match       97.7%;  Score 2697;  DB 12;  Length 543;
Best Local Similarity 100.0%;  Pred. No. 2.3e-224;
Matches  526;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

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Qy   13 VAVPAAAPVCQPKSATNGQPPAPAPTPTPRLSISSRATVVARMEGTSQGGLQTVMKWKTV  72
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Db   18 VAVPAAAPVCQPKSATNGQPPAPAPTPTPRLSISSRATVVARMEGTSQGGLQTVMKWKTV  77

Qy   73 VAIFVVVVYLVTGGLVFRALEQPFESSQKNTIALEKAEFLRDHVCVSPQELETLIQHAL  132
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   78 VAIFVVVVYLVTGGLVFRALEQPFESSQKNTIALEKAEFLRDHVCVSPQELETLIQHAL  137

Qy  133 DADNAGVSPIGNSSNNSSHWDLGSAFFAGTVITTIGYGNIAPSTEGGKIFCILYAIFGI  192
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  138 DADNAGVSPIGNSSNNSSHWDLGSAFFAGTVITTIGYGNIAPSTEGGKIFCILYAIFGI  197

Qy  193 PLFGFLLAGIGDQLGTIFGKSIARVEKVFRKKQVSQTKIRVISTILFILAGCIVFVTIPA 252
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  198 PLFGFLLAGIGDQLGTIFGKSIARVEKVFRKKQVSQTKIRVISTILFILAGCIVFVTIPA 257

Qy  253 VIFKYIEGWTALESIYFVVVTLTTVGFGDFVAGGNAGINYREWYKPLVWFWILVGLAYFA 312
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  258 VIFKYIEGWTALESIYFVVVTLTTVGFGDFVAGGNAGINYREWYKPLVWFWILVGLAYFA 317

Qy  313 AVLSMIGDWLRVLSKKTKEEVGEIKAHAAEWKANVTAEFRETRRRLSVEIHDKLQRAATI 372
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  318 AVLSMIGDWLRVLSKKTKEEVGEIKAHAAEWKANVTAEFRETRRRLSVEIHDKLQRAATI 377

Qy  373 RSMERRRLGLDQRAHSLDMLSPEKRSVFAALDTGRFKASSQESINNRPNNLRLKGPEQLN 432
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  378 RSMERRRLGLDQRAHSLDMLSPEKRSVFAALDTGRFKASSQESINNRPNNLRLKGPEQLN 437

Qy  433 KHGQGASEDNIINKFGSTSRLTKRKNDLKKTLPEDVQKIYKTFRNYSLDEEKKEETEK   492
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  438 KHGQGASEDNIINKFGSTSRLTKRKNDLKKTLPEDVQKIYKTFRNYSLDEEKKEETEK   497

Qy  493 MCNSDNSSTAMLTDCIQQHAELENGMIPTDTKDREPENNSLLEDRN 538
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Db  498 MCNSDNSSTAMLTDCIQQHAELENGMIPTDTKDREPENNSLLEDRN 543
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RESULT 6
US-10-332-175-2
; Sequence 2, Application US/10332175
; Publication No. US2003017634A1
; GENERAL INFORMATION:
; APPLICANT: Yamanouchi Pharmaceutical Co., Ltd.
; TITLE OF INVENTION: No. US2003017634A1e1 potassium channel
; FILE REFERENCE: Y0133PCT-666
; CURRENT APPLICATION NUMBER: US/10/332,175
; CURRENT FILING DATE: 2003-01-07
; PRIOR APPLICATION NUMBER: JP 2000-396020
; PRIOR FILING DATE: 2000-12-26
; NUMBER OF SEQ ID NOS: 6
; SEQ ID NO 2
; LENGTH: 543
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-332-175-2

Query Match       97.7%;  Score 2697;  DB 14;  Length 543;
Best Local Similarity 100.0%;  Pred. No. 2.3e-224;
Matches  526;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

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Qy   13 VAVPAAAPVCQPKSATNGQPPAPAPTPTPRLSISSRATVVARMEGTSQGGLQTVMKWKTV  72
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   18 VAVPAAAPVCQPKSATNGQPPAPAPTPTPRLSISSRATVVARMEGTSQGGLQTVMKWKTV  77

Qy   73 VAIFVVVVYLVTGGLVFRALEQPFESSQKNTIALEKAEFLRDHVCVSPQELETLIQHAL  132
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   78 VAIFVVVVYLVTGGLVFRALEQPFESSQKNTIALEKAEFLRDHVCVSPQELETLIQHAL  137
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RESULT 7
US-10-332-447-10
; Sequence 10, Application US/10332447
; Publication No. US2004005325A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.; RAUMANN, Brigitte E.;
; APPLICANT: THORNTON, Michael; DING, Li; YUE, Henry;
; APPLICANT: TANG, Y.Tom; HARLAND, Lee; BURFORD, Neil;
; APPLICANT: GREENE, Barrie D.; SANJANWALA, Madhu S.;
; APPLICANT: BAUGHN, Mariah R.; YAO, Monique G.; YANG, Junming;
; APPLICANT: ARVIZU, Chandra S.; GANDHI, Ameena R.;
; APPLICANT: HAFALIA, April J.A.; TRIBOULEY, Catherine M.;
; APPLICANT: WALIA, Narinder K.; AU-YOUNG, Janice;
; APPLICANT: WALSH, Roderick T.; RAMKUMAR, Jayalaxmi;
; APPLICANT: LU, Yan; LU, Dyung Aina M.; AZIMZAI, Yalda;
; APPLICANT: LAL, Preeti; ELLIOTT, Vicki S.; NGUYEN, Danniel B.;
; APPLICANT: XU, Yuning; SEILHAMER, Jeffrey J.; BOROWSKY, Mark L.;
; APPLICANT: KHAN, Farrah A.; KEARNEY, Liam; THANGAVELU, Kavitha;
; APPLICANT: DAS, Debopriya; POLICKY, Jennifer L.
; TITLE OF INVENTION: TRANSPORTERS AND ION CHANNELS
; FILE REFERENCE: PI-0149 USN
; CURRENT APPLICATION NUMBER: US/10/332,447
; CURRENT FILING DATE: 2003-01-07
; PRIOR APPLICATION NUMBER: US 60/216,547
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/218,232
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/220,112
; PRIOR FILING DATE: 2000-07-21
; PRIOR APPLICATION NUMBER: US 60/221,839
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PERL Program
; SEQ ID NO 10
; LENGTH: 724
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US2004005325A1 747272BCD1
US-10-332-447-10

Query Match       96.3%;  Score 2657.5;  DB 12;  Length 724;

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Qy  133 DADNAGVSPIGNSSNNSSHWDLGSAFFAGTVITTIGYGNIAPSTEGGKIFCILYAIFGI  192
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Db  138 DADNAGVSPIGNSSNNSSHWDLGSAFFAGTVITTIGYGNIAPSTEGGKIFCILYAIFGI  197

Qy  193 PLFGFLLAGIGDQLGTIFGKSIARVEKVFRKKQVSQTKIRVISTILFILAGCIVFVTIPA 252
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  198 PLFGFLLAGIGDQLGTIFGKSIARVEKVFRKKQVSQTKIRVISTILFILAGCIVFVTIPA 257

Qy  253 VIFKYIEGWTALESIYFVVVTLTTVGFGDFVAGGNAGINYREWYKPLVWFWILVGLAYFA 312
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  258 VIFKYIEGWTALESIYFVVVTLTTVGFGDFVAGGNAGINYREWYKPLVWFWILVGLAYFA 317

Qy  313 AVLSMIGDWLRVLSKKTKEEVGEIKAHAAEWKANVTAEFRETRRRLSVEIHDKLQRAATI 372
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Db  318 AVLSMIGDWLRVLSKKTKEEVGEIKAHAAEWKANVTAEFRETRRRLSVEIHDKLQRAATI 377

Qy  373 RSMERRRLGLDQRAHSLDMLSPEKRSVFAALDTGRFKASSQESINNRPNNLRLKGPEQLN 432
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Db  378 RSMERRRLGLDQRAHSLDMLSPEKRSVFAALDTGRFKASSQESINNRPNNLRLKGPEQLN 437

Qy  433 KHGQGASEDNIINKFGSTSRLTKRKNDLKKTLPEDVQKIYKTFRNYSLDEEKKEETEK   492
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  438 KHGQGASEDNIINKFGSTSRLTKRKNDLKKTLPEDVQKIYKTFRNYSLDEEKKEETEK   497

Qy  493 MCNSDNSSTAMLTDCIQQHAELENGMIPTDTKDREPENNSLLEDRN 538
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Db  498 MCNSDNSSTAMLTDCIQQHAELENGMIPTDTKDREPENNSLLEDRN 543
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Best Local Similarity 98.7%;  Pred. No. 9.5e-221;
Matches 523;  Conservative 1;  Mismatches 1;  Indels 5;  Gaps 2;

Qy   13  VAVPAAAPVCQPKSATNGQPPAPAPTPTPRLSISSRATVVARMEGTSQGGLQTVMKWKTV   72
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  196  VAVPAAAPVCQPKSATNGQPPAPAPTPTPRLSISSRATVVARMEGTSQGGLQTVMKWKTV  255

Qy   73  VAIFVVVVYLVTGGLVFRALEQPFESSQKNTIALEKAEFLRDHVCVSPQELETLIQHAL  132
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  256  VAIFVVVVYLVTGGLVFRALEQPFESSQKNTIALEKAEFLRDHVCVSPQELETLIQHAL  315

Qy  133  DADNAGVSPIGNSSNNSSHWDLGSAFFFAGTVITTIGYGNIAPSTEGGKIFCILYAIFGI  192
         |||||||||| |||||||||||||||||||||||::||||||||||||||||||||||||
Db  316  DADNAGVSPI-GNSSNNSSHWDLGSAFFFAGTVITTM-YGNIAPSTEGGKIFCILYAIFGI  374

Qy  193  PLFGFLLAGIGDQLGTIFGKSIARVEKVFRKKQVSQTKIRVISTILFILAGCIVFVTIPA  252
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  375  PLFGFLLAGIGDQLGTIFGKSIARVEKVFRKKQVSQTKIRVISTILFILAGCIVFVTIPA  434

Qy  253  VIFKYIEGWTALESIYFVVVTLTTVGFGDFVA----GGNAGINYREWYKPLVWFWILVGL  308
         ||||||||||||||||||||||||||||||||    |:||||||||||||||||||||||
Db  435  VIFKYIEGWTALESIYFVVVTLTTVGFGDFVAVVVFRGNAGINYREWYKPLVWFWILVGL  494

Qy  309  AYFAAVLSMIGDWLRVLSKKTKEEVGEIKAHAAEWKANVTAEFRETRRRLSVEIHDKLQR  368
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  495  AYFAAVLSMIGDWLRVLSKKTKEEVGEIKAHAAEWKANVTAEFRETRRRLSVEIHDKLQR  554

Qy  369  AATIRSMERRRLGLDQRAHSLDMLSPEKRSVFAALDTGRFKASSQESINNRPNNLRLKGP  428
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  555  AATIRSMERRRLGLDQRAHSLDMLSPEKRSVFAALDTGRFKASSQESINNRPNNLRLKGP  614

Qy  429  EQLNKHGQGASEDNIINKFGSTSRLTKRKNKDLKKTLPEDVQKIYKTFRNYSLDEEKKEE  488
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  615  EQLNKHGQGASEDNIINKFGSTSRLTKRKNKDLKKTLPEDVQKIYKTFRNYSLDEEKKEE  674

Qy  489  ETEKMCNSDNSSTAMLTDCIQQHAELENGMIPTDTKDREPENNSLLEDRN  538
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Db  675  ETEKMCNSDNSSTAMLTDCIQQHAELENGMIPTDTKDREPENNSLLEDRN  724
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RESULT 8
US-09-729-920-5
; Sequence 5, Application US/09729920
; Patent No. US2002010311SA1
; GENERAL INFORMATION:
; APPLICANT: GUEGLER, Karl et al
; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CL000858
; CURRENT APPLICATION NUMBER: US/09/729,920
; CURRENT FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 538
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-729-920-5

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Query Match 92.8%;  Score 2560.5;  DB 9;
Best Local Similarity 95.4%;  Pred. No. 1.5e-212;
Matches 503;  Conservative 9;  Mismatches 8;  Indels 7;  Gaps 2;

Qy   13  VAVPAAA-PVCQPKSATNGQPPAPAPTPTPRLSISSRATVVARMEGTSQGGLQTVMKWKT   71
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Db   18  VAVPAAAPPVCQPKSATNGH-----HEVPRLSISSRATVVARMEGASQGGLQTVMKWKT   71

Qy   72  VVAIFVVVVYLVTGGLVFRALEQPFESSQKNTIALEKAEFLRDHVCVSPQELETLIQHA  131
         ||:|||||||||||||||||||||||||||||||||||||||||:|||||||||||||||
Db   72  VVAIFVVVVYLVTGGLVFRALEQPFESSQKNTIALEKAEFLRDHICVSPQELETLIQHA  131

Qy  132  LDADNAGVSPIGNSSNNSSHWDLGSAFFFAGTVITTIGYGNIAPSTEGGKIFCILYAIFG  191
         |||||||||| ||||||||:|||||||||||||||||||||||||||||||||||||||||
Db  132  LDADNAGVSPVGNSSNNSSSHWDLGSAFFFAGTVITTIGYGNIAPSTEGGKIFCILYAIFG  191

Qy  192  IPLFGFLLAGIGDQLGTIFGKSIARVEKVFRKKQVSQTKIRVISTILFILAGCIVFVTIP  251
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  192  IPLFGFLLAGIGDQLGTIFGKSIARVEKVFRKKQVSQTKIRVISTILFILAGCIVFVTIP  251

Qy  252  AVIFKYIEGWTALESIYFVVVTLTTVGFGDFVAGGNAGINYREWYKPLVWFWILVGLAYF  311
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  252  AVIFKYIEGWTALESIYFVVVTLTTVGFGDFVAGGNAGINYREWYKPLVWFWILVGLAYF  311

Qy  312  AAVLSMIGDWLRVLSKKTKEEVGEIKAHAAEWKANVTAEFRETRRRLSVEIHDKLQRAAT  371
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  312  AAVLSMIGDWLRVLSKKTKEEVGEIKAHAAEWKANVTAEFRETRRRLSVEIHDKLQRAAT  371

Qy  372  IRSMERRRLGLDQRAHSLDMLSPEKRSVFAALDTGRFKASSQESINNRPNNLRLKGPEQL  431
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  372  IRSMERRRLGLDQRAHSLDMLSPEKRSVFAALDTGRFKASSQESINNRPNNLRLKGPEQL  431

Qy  432  NKHGQGASEDNIINKFGSTSRLTKRKNKDLKKTLPEDVQKIYKTFRNYSLDEEKKEEETE  491
         ||||||||||||||||||||:|||||||||||||||||||||||||||||||||||:|||
Db  432  NKHGQGASEDNIINKFGSTSKLTKRKNKDLKKTLPEDVQKIYKTFRNYSLDEEKKEDETE  491

Qy  492  KMCNSDNSSTAMLTDCIQQHAELENGMIPTDTKDREPENNSLLEDRN  538
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Db  492  KMCNSDNSSTAMLTECIQQQAEMENGMVPDMDTKDQGLENNSLLEDRN  538
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RESULT 9
US-09-828-746-6
; Sequence 6, Application US/09828746
; Patent No. US2002028485A1
; GENERAL INFORMATION:
; APPLICANT: Helen Jane Meadows
; APPLICANT: Conrad Gerald Chapman
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP-30031-D1
; CURRENT APPLICATION NUMBER: US/09/828,746
; CURRENT FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: US 09/236,080
; PRIOR FILING DATE: 1999-01-25
; PRIOR APPLICATION NUMBER: EP 98300570.3
; PRIOR FILING DATE: 1998-01-27
; PRIOR APPLICATION NUMBER: UK 9822135.1
; PRIOR FILING DATE: 1998-10-09
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 411
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-828-746-6

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Query Match 45.2%;  Score 1248.5;  DB 9;  Length 411;
Best Local Similarity 64.3%;  Pred. No. 3.4e-99;
Matches 247;  Conservative 53;  Mismatches 67;  Indels 17;  Gaps 5;

Qy   17  AAAPVCQPKSATNGQPPAPAPTPTPRLSISSRATVVA-RMEGTSQGGLQTVMKWKTVVAI   75
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Db    2  AAPDLLDPKSA---------AQNSKPRLSFSSKPTVLASRVESDS---AINVMKWKTVSTI   50

Qy   76  FVVVVYLVTGGLVFRALEQPFESSQKNTIALEKAEFLRDHVCVSPQELETLIQHALDAD  135
         | ||::||||||||  || :              |||::||||||||||::|||||  :
Db   51  FLVVVLYLIIGAAVFKALEQPEISQRTTIVIQKQTFIAQHACVNSTELEDLIQQIVAAI  110

Qy  136  NAGVSPIGNSSNNSSHWDLGSAFFFAGTVITTIGYGNIAPSTEGGKIFCILYAIFGPLF  195
         |||::|||| |||| :||:||:|||||||||||:|:|:| |    ||||:|||| :| |||
Db  111  NAGIIPLGNSNQVSHWDLGSSFFFFAGTVITTIGFGNISPRTEGGKIFCIIYALLGIPLF  170

Qy  196  GFLLAGIGDQLGTIFGKSIARVEKVFRKKQVSQTKIRVISTILFILAGCIVFVTIPAVIF  255
         ||||||:||:||||||| ||:||:  |   ||:|||||:||:||||  ::|||::|||||
Db  171  GFLLAGVGDQLGTIFGKGIAKVEDTFIKWNVSQTKIRIISTIIFILFGCVLFVALPAVIF  230
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Qy    256  KYIEGWTALESIYFVVVTLTTVGPGDFVAGGNAGINYREWYKPLVWFWILVGLAYFAAVL  315
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Db    256  KYIEGWTALESIYFVVVTLTTVGPGDFVAGGNAGINYREWYKPLVWFWILVGLAYFAAVL  315

Qy    231  KHIEGWSALDAIYFVVITLTTIGFGDYVAGG-SDIEYLDFYKPVWFWILVGLAYFAAVL   289
                |||||||||||||||||||||| ||||| :||||||||||||||||||||||||
Db    231  KHIEGWSALDAIYFVVITLTTIGFGDYVAGG-SDIEYLDFYKPVWFWILVGLAYFAAVL   289

Qy    316  SMIGDWLRVLSKKTKEEVGEIKAHAAEWKANVTAEFRETRRRLSVEIHDKLQRAATIRSM  375
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Db    316  SMIGDWLRVISKKTKEEVGEGFRAHAAAEWTANVTAEFKETRRRLSVEIYDKFQRATSV---  346

Qy    376  ERRRLGLDQRAHSLDMLSPEKRSV  399
                :| |  :   :||  :|:|
Db    374  -SME---------RRRLGLDQRAHSLDMLSP  394

Qy    347  -KRKLSAELAGNHNQELTPCRRTL  369
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Db    350  LSAELAGNHNQELTPCRRTLSVNHLTNERDVLPP  383


RESULT 10
US-09-892-360-18
; Sequence 18, Application US/09892360
; Publication No. US20040101833A1
; GENERAL INFORMATION:
;   APPLICANT: LAZDUNSKI, MICHEL
;   APPLICANT: LESAGE, FLORIAN
;   APPLICANT: ROMEY, GEORGES
;   TITLE OF INVENTION: HUMAN TREK2, A STRETCH-AND ARACHIDONIC ACID-SENSITIVE
;   TITLE OF INVENTION: K+ CHANNEL ACTIVATED BY INHALATIONAL ANESTHETICS AND
;   TITLE OF INVENTION: RILUZOLE
;   FILE REFERENCE: 1256-R-00
;   CURRENT APPLICATION NUMBER: US/09/892,360
;   CURRENT FILING DATE: 2001-05-27
;   PRIOR APPLICATION NUMBER: 60/214,559
;   PRIOR FILING DATE: 2000-06-27
;   NUMBER OF SEQ ID NOS: 25
;   SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
;   LENGTH: 411
;   TYPE: PRT
;   ORGANISM: Mus musculus
US-09-892-360-18

Query Match             45.0%;  Score 1243;  DB 12;  Length 411;
Best Local Similarity   62.7%;  Pred. No. 1e-98;
Matches   247;  Conservative  54;  Mismatches  65;  Indels  28;  Gaps  6;

Qy     17  AAAPVCQPKSATNGQPPAPAPTPTPRLSISSRATVVA-RMEGTSQGGLQTVMKWKTVVAI   75
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Db      2  AAPDLLDPKSA-------AQNSKPRLSFSTKPTVLASRVESDT---TINVMKWKTVSTI   50

Qy     76  FVVVVVYLVTGGLVFRALEQPFESSQKNTIALEKAEFLRDHVCVSPQELETLIQHALDAD  135
               |:||:|||:| || |||: ||  :|:  ||: || :|
Db     51  FLVVVLYLIIGATVFKALEQPHEISQRTTIVIQKQTFISQHSCVNSTELDELIQQIVAAI  110

Qy    136  NAGVSPIGNSSNNSSHWDLGSAFFFAGTVITTIGYGNIAPSTEGGKIFCILYAIFGIPLF  195
               || |:|||| : :||||||||||||:|||||:|| || ||:||||||:|:||:||||
Db    111  NAGIIPLGNTSNQISHWDLGSSFFFAGTVITTIGFGNISPRTEGGKIFCIIYALLGIPLF  170

Qy    196  GFLLAGIGDQLGTIFGKSIARVEKVFRKKQVSQTKIRVISTLFILAGCIVFVTIPAVIF   255
               |||||:||||||||||||:||:||:::|||||||||:|||:||| |::|| ||:|:
Db    171  GFLLAGVGDQLGTIFGKGIAKVEDTFIKWNVSQTKIRIISTIIFILFGCVLFVALPAIIF  230

Qy    256  KYIEGWTALESIYFVVVTLTTVGPGDFVAGGNAGINYREWYKPLVWFWILVGLAYFAAVL  315
                |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    231  KHIEGWSALDAIYFVVITLTTIGFGDYVAGG-SDIEYLDFYKPVWFWILVGLAYFAAVL   289

Qy    316  SMIGDWLRVLSKKTKEEVGEIKAHAAEWKANVTAEFRETRRRLSVEIHDKLQRAATIR--  373
               ||||||||:|||||||||| :||||| :|||||||||||||||||||:|||||:
Db    290  SMIGDWLRVISKKTKEEVGEGFRAHAAAEWTANVTAEFKETRRRLSVEIYDKFQRATSIKRK  349

Qy    374  -SME---------RRRLGLDQRAHSLDMLSP  394
               :|   | |  :||  :|:||||:|
Db    350  LSAELAGNHNQELTPCRRTLSVNHLTNERDVLPP  383


RESULT 11
US-09-828-746-2
; Sequence 2, Application US/09828746
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; Patent No. US20020028485A1
; GENERAL INFORMATION:
;   APPLICANT: Helen Jane Meadows
;   APPLICANT: Conrad Gerald Chapman
;   TITLE OF INVENTION: NOVEL COMPOUNDS
;   FILE REFERENCE: GP-30031-D1
;   CURRENT APPLICATION NUMBER: US/09/828,746
;   CURRENT FILING DATE: 2001-04-09
;   PRIOR APPLICATION NUMBER: US 09/236,080
;   PRIOR FILING DATE: 1999-01-25
;   PRIOR APPLICATION NUMBER: EP 98300570.3
;   PRIOR FILING DATE: 1998-01-27
;   PRIOR APPLICATION NUMBER: UK 9822135.1
;   PRIOR FILING DATE: 1998-10-09
;   NUMBER OF SEQ ID NOS: 6
;   SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2
;   LENGTH: 411
;   TYPE: PRT
;   ORGANISM: HOMO SAPIENS
US-09-828-746-2

Query Match             45.0%;  Score 1242.5;  DB 9;  Length 411;
Best Local Similarity   63.5%;  Pred. No. 1.1e-98;
Matches   244;  Conservative  57;  Mismatches  66;  Indels  17;  Gaps  5;

Qy     17  AAAPVCQPKSATNGQPPAPAPTPTPRLSISSRATVVA-RMEGTSQGGLQTVMKWKTVVAI   75
               || |||| |   :   |::|
Db      2  AAPDLLDPKSA-------AQNSKPRLSFSTKPTVLASRVESDT---TINVMKWKTVSTI   50

Qy     76  FVVVVVYLVTGGLVFRALEQPFESSQKNTIALEKAEFLRDHVCVSPQELETLIQHALDAD  135
               |:||:|||:| || |||: ||  :|:  ||: || :|
Db     51  FLVVVLYLIIGATVFKALEQPHEISQRTTIVIQKQTFISQHSCVNSTELDELIQQIVAAI  110

Qy    136  NAGVSPIGNSSNNSSHWDLGSAFFFAGTVITTIGYGNIAPSTEGGKIFCILYAIFGIPLF  195
               || |:|||| : :||||||||||||:|||||:|| || ||:||||||:|:||:||||
Db    111  NAGIIPLGNTSNQISHWDLGSSFFFAGTVITTIGFGNISPRTEGGKIFCIIYALLGIPLF  170

Qy    196  GFLLAGIGDQLGTIFGKSIARVEKVFRKKQVSQTKIRVISTLFILAGCIVFVTIPAVIF   255
               |||||:||||||||||||:||:||:::|||||||||:|||:||| |::|| ||:|:
Db    171  GFLLAGVGDQLGTIFGKGIAKVEDTFIKWNVSQTKIRIISTIIFILFGCVLFVALPAIIF  230

Qy    256  KYIEGWTALESIYFVVVTLTTVGPGDFVAGGNAGINYREWYKPLVWFWILVGLAYFAAVL  315
                |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    231  KHIEGWSALDAIYFVVITLTTIGFGDYVAGG-SDIEYLDFYKPVWFWILVGLAYFAAVL   289

Qy    316  SMIGDWLRVLSKKTKEEVGEIKAHAAEWKANVTAEFRETRRRLSVEIHDKLQRAATIRSM  375
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Db    290  SMIGDWLRVISKKTKEEVGEGFRAHAAAEWTANVTAEFKETRRRLSVEIYDKFQRATSI---  346

Qy    376  ERRRLGLDQRAHSLDMLSPEKRSV  399
               :| |  :   :||  :|:|
Db    347  -KRKLSAELAGNHNQELTPCRRTL  369


RESULT 12
US-10-121-746-83
; Sequence 83, Application US/10121746
; Publication No. US2003036648A1
; GENERAL INFORMATION:
;   APPLICANT: Miller, Andrew P.
;   APPLICANT: Curran, Mark Edward
;   APPLICANT: Hu, Ping
;   APPLICANT: Rutter, Marc
;   APPLICANT: Wang, Jian-Wang
;   TITLE OF INVENTION: No. US20030036648A1el Human Potassium Channels
;   FILE REFERENCE: SEQ-15P
;   CURRENT APPLICATION NUMBER: US/10/121,746
;   CURRENT FILING DATE: 2002-04-11
;   PRIOR APPLICATION NUMBER: US/09/336,643A
;   PRIOR FILING DATE: 1999-06-18
;   PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/076,687
;   PRIOR FILING DATE: EARLIER FILING DATE: 1998-08-07
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; FEATURE:
; OTHER INFORMATION: TREK-1
US-09-939-484-8

Query Match    44.9%;   Score 1238.5;  DB 9;  Length 370;
Best Local Similarity    64.2%;  Pred. No. 2.2e-98;
Matches   246;  Conservative    52;  Mismatches   68;  Indels   17;  Gaps    5;

Qy     17  AAAPVCQPKSATNGQPPAPATPTPRLSISSRATVVA-RMEGTSQGGLQTVMKWKTVVAI   75
               ||::|:|        |||:|:|::: ||||| ||||||||||||||||
Db      2  AAPDLLDPKSA--------AQNSKPRLSFSSKPTVLASRVESDS--AINVMKWKTVSTI   50

Qy     76  FVVVVVLVTGGLVFRALEQPPESSQKNTIALEKAEFLRDHVCVSPQELETLIQHALDAD  135
               |::||::|:  ||:|:||   || :::|: |   ||: |::|||:||||||||
Db     51  FLVVVLYLIIGAAVFKALEQPQEISQRTTIVIQKQTFIAQHACVNSTELDELIQQIVAAI  110

Qy    136  NAGVSPIGNSSNNSSHWDLGSAFFFAGTVITTIGYGNIAPSTEGGKIFCILYAIFGIPLF  195
               ||| |:|||: |||||||  ||| :|:|| |||||||:||||||| |||:||:
Db    111  NAGIIPLGNSSNQVSHWDLGSSFFFAGTVITTIGFGNISPRTEGGKIFCIIYALLGIPLE  170

Qy    196  GFLLAGIGDQLGTIFGKSIARVEKVFRKKQVSQTKIRVISTILFILAGCIVFVTIPAVIF  255
               |||||||||||||||| :|||| :||:||||||||||||:||| :::| ||:||||
Db    171  GFLLAGVGDQLGTIFGKGIAKVEDTFIKWNVSQTKIRIISTIIFILFGCVLFVALPAVIF  230

Qy    256  KYIEGWTALESIYFVVVLTTVGFGDFVAGGNAGINYREWYKPLVWFWILVGLAYFAAVL  315
               |:|||:||:|||||||:||: |:|||||| :  |:: :||:|||||||||:||||
Db    231  KHIEGWSALDAIYFVVITLTTIGFGDYVAGG-SDIEYLDFYKPVVWFWILVGLAYFAAVL  289

Qy    316  SMIGDWLRVLSKKTKEEVGEIKAHAAEWKANVTAEFRETRRRLSVEIHDKLQRAATIRSM  375
               ||||||||| |::|||||||| :  |:|||:|||:||:|||||||:|||||:: :
Db    290  SMIGDWLRVISKKTKEEVGEFRAHAAEWTANVTAEFKETRRRLSVEIYDKFQRATSV---  346

Qy    376  ERRRLGLDQRAHSLDMLSPEKRS  398
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Db    347  -KRKLSAELAGNHNQELTPCMRT  368

RESULT 14
US-09-939-483-8
; Sequence 8, Application US/09939483
; Patent No. US20020094558A1
; GENERAL INFORMATION:
; APPLICANT: Duprat, Fabrice
; APPLICANT: Lesage, Florian
; APPLICANT: Fink, Michel
; APPLICANT: Lazdunski, Michel
; TITLE OF INVENTION: FAMILY OF MAMMALIAN POTASSIUM CHANNELS, THEIR CLONING
; TITLE OF INVENTION: AND THEIR USE, ESPECIALLY FOR THE SCREENING OF DRUGS
; FILE REFERENCE: 1201-CIP-DIV-2-00
; CURRENT APPLICATION NUMBER: US/09/939,483
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 09/144,914
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 08/749,816
; PRIOR FILING DATE: 1996-11-15
; PRIOR APPLICATION NUMBER: 60/095,234
; PRIOR FILING DATE: 1998-08-04
; PRIOR APPLICATION NUMBER: FR 96/01565
; PRIOR FILING DATE: 1996-02-08
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.0
;
; SEQ ID NO 8
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Murine
; FEATURE:
; OTHER INFORMATION: TREK-1
US-09-939-483-8

Query Match    44.9%;   Score 1238.5;  DB 9;  Length 370;
Best Local Similarity    64.2%;  Pred. No. 2.2e-98;
Matches   246;  Conservative    52;  Mismatches   68;  Indels   17;  Gaps    5;

; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/116,448
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-19
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: PCT/US99/03826
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-22
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 83
; LENGTH: 411
; TYPE: PRT
; ORGANISM: H. sapiens
US-10-121-746-83

Query Match    45.0%;   Score 1242.5;  DB 14;  Length 411;
Best Local Similarity    63.5%;  Pred. No. 1.1e-98;
Matches   244;  Conservative    57;  Mismatches   66;  Indels   17;  Gaps    5;

Qy     17  AAAPVCQPKSATNGQPPAPATPTPRLSISSRATVVA-RMEGTSQGGLQTVMKWKTVVAI   75
               ||::|:|        |||:|:|::: ||||| |||||||||
Db      2  AAPDLLDPKSA--------AQNSKPRLSFSTKPTVLASRVESDT---TINVMKWKTVSTI   50

Qy     76  FVVVVVLVTGGLVFRALEQPPESSQKNTIALEKAEFLRDHVCVSPQELETLIQHALDAD  135
               |::||::|:  ||:|:||   || :::|: |   ||: |::|||:||||||||
Db     51  FLVVVLYLIIGATVFKALEQPHEISQRTTIVIQKQTFISQHSCVNSTELDELIQQIVAAI  110

Qy    136  NAGVSPIGNSSNNSSHWDLGSAFFFAGTVITTIGYGNIAPSTEGGKIFCILYAIFGIPLF  195
               ||| |:|||: |||||||  ||| :|:|| |||||||:||||||| |||:||:
Db    111  NAGIIPLGNTSNQISHWDLGSSFFFAGTVITTIGFGNISPRTEGGKIFCIIYALLGIPLF  170

Qy    196  GFLLAGIGDQLGTIFGKSIARVEKVFRKKQVSQTKIRVISTILFILAGCIVFVTIPAVIF  255
               |||||||||||||||| :|||| :||:||||||||||||:||| :::| ||:||||
Db    171  GFLLAGVGDQLGTIFGKGIAKVEDTFIKWNVSQTKIRIISTIIFILFGCVLFVALPAIIF  230

Qy    256  KYIEGWTALESIYFVVVLTTVGFGDFVAGGNAGINYREWYKPLVWFWILVGLAYFAAVL  315
               |:|||:||:|||||||:||: |:|||||| :  |:: :||:|||||||||:||||
Db    231  KHIEGWSALDAIYFVVITLTTIGFGDYVAGG-SDIEYLDFYKPVVWFWILVGLAYFAAVL  289

Qy    316  SMIGDWLRVLSKKTKEEVGEIKAHAAEWKANVTAEFRETRRRLSVEIHDKLQRAATIRSM  375
               ||||||||| |::|||||||| :  |:|||:|||:||:||||||||:|||||:: :
Db    290  SMIGDWLRVISKKTKEEVGEFRAHAAEWTANVTAEFKETRRRLSVEIYDKFQRATSI---  346

Qy    376  ERRRLGLDQRAHSLDMLSPEKRSV  399
               :|:|  :||  :: |
Db    347  -KRKLSAELAGNHNQELTPCRRTL  369

RESULT 13
US-09-939-484-8
; Sequence 8, Application US/09939484
; Patent No. US20020032322A1
; GENERAL INFORMATION:
; APPLICANT: Duprat, Fabrice
; APPLICANT: Lesage, Florian
; APPLICANT: Fink, Michel
; APPLICANT: Lazdunski, Michel
; TITLE OF INVENTION: FAMILY OF MAMMALIAN POTASSIUM CHANNELS, THEIR CLONING
; TITLE OF INVENTION: AND THEIR USE, ESPECIALLY FOR THE SCREENING OF DRUGS
; FILE REFERENCE: 1201-CIP-DIV-00
; CURRENT APPLICATION NUMBER: US/09/939,484
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 09/144,914
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 08/749,816
; PRIOR FILING DATE: 1996-11-15
; PRIOR APPLICATION NUMBER: 60/095,234
; PRIOR FILING DATE: 1998-08-04
; PRIOR APPLICATION NUMBER: FR 96/01565
; PRIOR FILING DATE: 1996-02-08
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.0
;
; SEQ ID NO 8
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Murine

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Qy   17  AAAPVCQPKSATNGQPPAPAPTPTPRLSISSRATVVA-RMEGTSQGGLQTVMKWKTVVAI  75
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Db    2  AAPDLLDPKSA------AQNSKPRLSFSSKPTVLASRVESDS---AINVMKWKTVSTI  50

Qy   76  FVVVVYLVTGGLVFRALEQPFESSQKNTIALEKAEFLRDHVCVSPQELETLIQHALDAD  135
         |:||:||:|| ||:||||||| |:| || : ||| : ||| :| :
Db   51  FLVVVLYLIIGAAVFKALEQPEISQRTTIVIQKQTFIAQHACVNSTELDELIQQIVAAI  110

Qy  136  NAGVSPIGNSSNNSSHWDLGSAFFPAGTVITTIGYGNIAPSTEGGKIFCILYAIFGIPLF  195
         ||| :| |||||:|||||||||:||||||||||||:|||| |||||||||:||:||||:
Db  111  NAGIIPLGNSSNQVSHWDLGSSFFPAGTVITTIGFGNISPRTEGGKIFCIIYALLGIPLE  170

Qy  196  GFLLAGIGDQLGTIFGKSIARVEKVFRKKQVSQTKIRVISTILFILAGCIVFVTIPAVIF  255
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Db  171  GFLLAGVGDQLGTIFGKGIAKVEDTFIKWNVSQTKIRIISTIIFILFGCVLFVALPAVIF  230

Qy  256  KYIEGWTALESIYFVVVTLTTVGFGDFVAGGNAGINYREWYKPLVWFWILVGLAYFAAVL  315
         |:||||:||:.|||||.|||||||||:|||| .  :  :||| ||||||||||||||||
Db  231  KHIEGWSALDAIYFVVITLTTIGFGDYVAGG-SDIEYLDFYKPVVWFWILVGLAYFAAVL  289

Qy  316  SMIGDWLRVLSKKTKEEVGEIKAHAAEWKANVTAEFRETRRRLSVEIHDKLQRAATIRSM  375
         |||||||||:||||||||||::|||||||:|||||||:||||||||||:||:|||||:
Db  290  SMIGDWLRVISKKTKEEVGEFRAHAAEWTANVTAEFKETRRRLSVEIYDKFQRATSV---  346

Qy  376  ERRRLGLDQRAHSLDMLSPEKRS  398
          :|| | ||| | :|:
Db  347  -KRKLSAELAGNHNQELTPCMRT  368
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Qy   17  AAAPVCQPKSATNGQPPAPAPTPTPRLSISSRATVVA-RMEGTSQGGLQTVMKWKTVVAI  75
             |:|| |||| ||  || :| |:| :|  ||||||||||||
Db   17  AAPDLLDPKSA------AQNSKPRLSFSTKPTVLASRVESDT---TINVMKWKTVSTI  65

Qy   76  FVVVVYLVTGGLVFRALEQPFESSQKNTIALEKAEFLRDHVCVSPQELETLIQHALDAD  135
         |:||:||:|| ||:||||||| |:| :|| : ||| :| ::
Db   66  FLVVVLYLIIGATVFKALEQPHEISQRTTIVIQKQTFISQHSCVNSTELDELIQQIVAAI  125

Qy  136  NAGVSPIGNSSNNSSHWDLGSAFFPAGTVITTIGYGNIAPSTEGGKIFCILYAIFGIPLF  195
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Db  126  NAGIIPLGNTSNQISHWDLGSSFFFAGTVITTIGFGNISPRTEGGKIFCIIYALLGIPLF  185

Qy  196  GFLLAGIGDQLGTIFGKSIARVEKVFRKKQVSQTKIRVISTILFILAGCIVFVTIPAVIF  255
         ||||||:||||||||||.||.||:.||   |||||||:|||||||||| :|||:|||:||
Db  186  GFLLAGVGDQLGTIFGKGIAKVEDTFIKWNVSQTKIRIISTIIFILFGCVLFVALPAIIF  245

Qy  256  KYIEGWTALESIYFVVVTLTTVGFGDFVAGGNAGINYREWYKPLVWFWILVGLAYFAAVL  315
         |:||||:||:.|||||.|||||||||:|||| .  :  :||| ||||||||||||||||
Db  246  KHIEGWSALDAIYFVVITLTTIGFGDYVAGG-SDIEYLDFYKPVVWFWILVGLAYFAAVL  304

Qy  316  SMIGDWLRVLSKKTKEEVGEIKAHAAEWKANVTAEFRETRRRLSVEIHDKLQRAATIRSM  375
         ||||.|:|||:||||||||||::|||||||:|||||||:||||||||||:||:|||||:
Db  305  SMIGRLVRVISKKTKEEVGEFRAHAAEWTANVTAEFKETRRRLSVEIYDKFQRATSI---  361

Qy  376  ERRRLGLDQRAHSLDMLSPEKRSV  399
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Db  362  -KRKLSAELAGNHNQELTPCRRTL  384
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Search completed: June 29, 2004, 18:25:28
Job time : 51 secs

RESULT 15
US-08-816-011-45

Query Match    44.1%;  Score 1218.5;  DB 8;  Length 426;
Best Local Similarity  62.8%;  Pred. No. 1.4e-96;
Matches  241;  Conservative  58;  Mismatches  68;  Indels  17;  Gaps  5;

OM protein - protein search, using sw model

Copyright    GenCore version 5.1.6
Copyright (c) 1993 - 2004  Compugen Ltd.

Run on:    June 29, 2004, 18:15:42 ; Search time 21 Seconds
(without alignments)
2464.335 Million cell updates/sec

Title:         US-09-892-360-2
Perfect score: 2760
Sequence:      1 MFFLYTDFFLSLVAVPAAAP.........IPTDTKDREPENNSLLEDRN 538
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched:      283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters:      283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :    PIR_78:*
1: pirl:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query Match | Length | DB | ID | Description |
|---|---|---|---|---|---|---|
| 1 | 403 | 14.6 | 336 | 2 | S65566 | inward rectifier p |
| 2 | 329 | 11.9 | 330 | 2 | JC7703 | TASK-5 protein - h |
| 3 | 326 | 11.8 | 1001 | 2 | T13807 | potassium channel |
| 4 | 315.5 | 11.4 | 329 | 2 | T43509 | probable potassium |
| 5 | 307 | 11.1 | 336 | 2 | T32347 | outward rectifier |
| 6 | 300.5 | 10.9 | 364 | 2 | T43361 | probable potassium |
| 7 | 298.5 | 10.8 | 393 | 2 | T25392 | hypothetical prote |
| 8 | 298.5 | 10.8 | 1910 | 2 | H88124 | protein T12C9.3 [i |
| 9 | 290.5 | 10.5 | 334 | 2 | T19860 | hypothetical prote |
| 10 | 282.5 | 10.2 | 392 | 2 | T45032 | hypothetical prote |
| 11 | 268.5 | 9.7 | 522 | 2 | T24265 | hypothetical prote |
| 12 | 265.5 | 9.6 | 528 | 2 | T21834 | hypothetical prote |
| 13 | 264.5 | 9.6 | 444 | 2 | T26229 | hypothetical prote |
| 14 | 264 | 9.6 | 551 | 2 | T16426 | potassium channel |
| 15 | 264 | 9.6 | 555 | 2 | T43357 | hypothetical prote |
| 16 | 262.5 | 9.5 | 443 | 2 | T21598 | potassium channel |
| 17 | 260 | 9.4 | 461 | 2 | T43394 | hypothetical prote |
| 18 | 258.5 | 9.4 | 513 | 2 | T28933 | hypothetical prote |
| 19 | 255 | 9.2 | 452 | 2 | T21118 | hypothetical prote |
| 20 | 252.5 | 9.1 | 586 | 2 | T21683 | hypothetical prote |
| 21 | 248 | 9.0 | 325 | 2 | T15584 | hypothetical prote |
| 22 | 247 | 8.9 | 427 | 2 | T27681 | hypothetical prote |
| 23 | 245 | 8.9 | 1136 | 2 | T26953 | hypothetical prote |
| 24 | 244 | 8.8 | 504 | 2 | T22269 | probable potassium |
| 25 | 233.5 | 8.5 | 484 | 2 | T43529 | hypothetical prote |
| 26 | 233.5 | 8.5 | 519 | 2 | T16629 | hypothetical prote |
| 27 | 233.5 | 8.5 | 1539 | 2 | T30037 | hypothetical prote |
| 28 | 229.5 | 8.3 | 383 | 2 | T23182 | hypothetical prote |
| 29 | 227.5 | 8.2 | 307 | 2 | H89074 | protein twk-24 [lim |
| 30 | 224.5 | 8.1 | 524 | 2 | T23907 | hypothetical prote |
| 31 | 224.5 | 8.1 | 769 | 2 | T27550 | hypothetical prote |
| 32 | 221.5 | 8.0 | 643 | 2 | T26616 | hypothetical prote |
| 33 | 218 | 7.9 | 335 | 2 | S44635 | f22b7.7 protein - |
| 34 | 217.5 | 7.9 | 691 | 2 | S46585 | outward-rectifier |
| 35 | 216.5 | 7.8 | 576 | 2 | T43363 | potassium channel |
| 36 | 213.5 | 7.7 | 660 | 2 | T21551 | hypothetical prote |
| 37 | 213 | 7.7 | 569 | 2 | T43531 | probable potassium |
| 38 | 210.5 | 7.6 | 544 | 2 | T43364 | potassium channel |
| 39 | 208.5 | 7.6 | 485 | 2 | T24201 | hypothetical prote |
| 40 | 207.5 | 7.5 | 700 | 2 | T27364 | hypothetical prote |
| 41 | 204.5 | 7.4 | 550 | 2 | T22557 | hypothetical prote |
| 42 | 203.5 | 7.4 | 539 | 2 | T23700 | hypothetical prote |
| 43 | 202 | 7.3 | 681 | 2 | T19429 | hypothetical prote |
| 44 | 198 | 7.2 | 631 | 2 | T26232 | hypothetical prote |
| 45 | 189.5 | 6.9 | 475 | 2 | T27725 | hypothetical prote |

ALIGNMENTS

RESULT 1
S65566
inward rectifier potassium channel TWIK-1 - human
C;Species: Homo sapiens (man)
C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 05-Nov-1999
C;Accession: S65566
R;Lesage, F.; Guillemare, E.; Fink, M.; Duprat, F.; Lazdunski, M.; Romey, G.; Barhanin, J
EMBO J. 15, 1004-1011, 1996
A;Title: TWIK-1, a ubiquitous human weakly inward rectifying K(+) channel with a novel st
A;Reference number: S65566; MUID:96183184; PMID:8605869
A;Accession: S65566
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-336 <LES>
A;Cross-references: EMBL:U33632; NID:g1086490; PIDN:AAB01688.1; PID:g1086491

Query Match             14.6%;  Score 403;  DB 2;  Length 336;
Best Local Similarity   33.2%;  Pred. No. 1.1e-20;
Matches   95;  Conservative   53;  Mismatches  104;  Indels   34;  Gaps    9;

Qy     76 FVVV--VVYLVTGGLVFRALEQPFESSQKNTIALEKABFLRDHVCVSPQELETLIQHALD 133
             :|:  |||:|::||  ::|:|  : :| |  ||: :  :: ::|.
Db     25 FLVLGYLLYLVFGAVVFSSVELPYEDLLRQELRKLKRRFLEEHECLSEQLEQFLGRVLE 84

Qy    134 ADNAGVSPIGNSSNNSSHWDLGSAFFFAGTVITTIGYGNIAPSTEGGKIFCILYAIFGIP 193
            |||.|| ||||| ||: |||:||| ::||: |||| |||||...:||||:|:||||
Db     85 ASNYGVSVLSNASGN-WNMDFTSALFFASTVLSTGYGHTVPLSDGGKAFCIIYSVIGIP 143

Qy    194 LFGFLLAGIGDQLGTIFGKSIARVBKVFRKKQV--------SQTKIRVISTIL--FILA 242
            |::.:  :::|::|: :||: |: ||::|:
Db    144 FTLLFLTAV-------VQRITVHVTRRPVLYFHIRWGFSKQVVAIVHAVLLGFVTV 192

Qy    243 GCIVPVTIPAVIFKYIE-GWTALESIYFVVVTLLTTVGFGDFVAGGNAGINYREWKPLVW 301
            : :|  || ::   | :| ||  ||:   :|    |||| :|||    : :|
Db    193 SCFFF--IPAAVFSVLEDDWNFLESFYFCFISLSTIGLGDYVFGEGYNQXFRELYKIGIT 250

Qy    302 FWILVGLAYFAAVLSMIGDWLRVLSK-----KTKEEVGEIKAHAAE 342
            ::|:|||||  :::|: || :|:
Db    251 CYLLIGLIAMLVVLETFCE-LHELKKFPRKMFYVKKDKDEDQVHIIE 295

RESULT 2
JC7703
TASK-5 protein - human
C;Species: Homo sapiens (man)
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Nov-2001
C;Accession: JC7703
R;Kim, D.; Gnatenco, C.
Biochem. Biophys. Res. Commun. 284, 923-930, 2001
A;Title: TASK-5, a new member of the tandem-pore K+ channel family.
A;Reference number: JC7703; MUID:21303050; PMID:11409881
A;Accession: JC7703

A;Molecule type: DNA
A;Residues: 1-330 <KIM>
A;Cross-references: GB:AL118522
C;Comment: This protein, a new member of the tandem-pore K+ channel family with four tra
hormone secretion, but does not produce a functional plasma membrane K+ current by itsel
C;Genetics:
A;Gene: task-5
A;Map position: 20q12
C;Keywords: transmembrane protein
F;7-30/Domain: transmembrane segment #status predicted <TMS1>
F;107-128/Domain: transmembrane segment #status predicted <TMS2>
F;129-155/Region: hydrophobic cytoplasmic linker #status predicted
F;156-180/Domain: transmembrane segment #status predicted <TMS3>
F;224-240/Domain: transmembrane segment #status predicted <TMS4>

Query Match             11.9%;  Score 329;  DB 2;  Length 330;
Best Local Similarity   32.4%;  Pred. No. 1.6e-15;
Matches    85;  Conservative   46;  Mismatches   97;  Indels   34;  Gaps    9;

Qy     75 IFVVVVVLVTGGLVFRALEQPPESSQKNTIALEKAEPLRDHVCVSPQELETLIQHALDA 134
          : :|||::|||  ||||   |||:   :  :  :    :      : : ||||
Db     11 LVLCTLCYLLVGAAVFDALESEAESGRQR-LLVQKRGALRRKPGFSAEDYRELERLALQA 69

Qy    135 D--NAGVSPIGNSSNNSSHWDLGSAFFFAGTVITTIGYGNIAPSTEGGKIFCILYAIFGI 192
          |   :: ||||:|:|::||||||:|||||||||||:||||||||
Db     70 RQWKFPGSFYPFAITVITTIGYGHAAPGTDSGKVFCMFYALLGI 118

Qy    193 PLFGFLLAGIGDQLGTIFGKSIARVEKVFRKKQVSQTKIRVISTILFILAG---CIVFVT 249
          ||   ||||    || :|:  |      ||:  ::    :| ||||:||  ||||
Db    119 PLTLIVTFQSLGERLNAV--VRRL--LLAAKCCLGLRWTCVSTENLVVAGLLACAATLA 172

Qy    250 IPAVIFKYIEGWTALESIYFVVVTLTTVGFGDFVA--GGNAGINYREWYKPLVWFWILVG 307
          ||| ||||||||||||||:|:||||||||||||||     : ||| : :  | |  ||
Db    173 LGVAFSHFEGWTFFHAYYYCFTLTTIGFGDFVALQSGEA-LQRKLPYVAFSFLYILLG 231

Qy    308 LAYFAAVLSMI-------GDW 321
          | |||||:|
Db    232 LTVIGAFLNLVVLRFLVASADW 253

RESULT 3
T13807
potassium channel protein - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 17-Nov-2000
C;Accession: T13807
R;Goldstein, S.A.; Price, L.A.; Rosenthal, D.N.; Pausch, M.H.
Proc. Natl. Acad. Sci. U.S.A. 93, 13256-13261, 1996
A;Title: ORK1, a potassium-selective leak channel with two pore domains cloned from Dros
A;Reference number: 217770; MUID:97075152; PMID:8917578
A;Accession: T13807
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1001 <GOL>
A;Cross-references: EMBL:U55321; NID:g3808067; PIDN:AAC69250.1
C;Genetics:
A;Gene: ORK1
A;Cross-references: FlyBase:FBgn0017561
A;Map position: 1

Query Match             11.8%;  Score 326;  DB 2;  Length 1001;
Best Local Similarity   22.9%;  Pred. No. 1.1e-14;
Matches   123;  Conservative   93;  Mismatches  193;  Indels  128;  Gaps   20;

Qy     68 KWKTVVAIFVVVVVLVTGGLVFRALEQPPESSQKNTIALEKAEPLRDHVCVSPQELETL 127
          : :|  ||   || ||||:||||||   ||||   :   :      : : || :|
Db      5 RW---ILLLIFYISYLMFGAAIYYHEHGEEK------ISRAEQRKAQIAINEYLLEEL 54

Qy    128 ---------IQHALDADNAGVSPIGNSSNNSSHWDLGSAFFFAGTVITTIGYGNIAPS 176
                   :      :: ||||:|:|::||||||:||||||||||:||||||||
Db     55 GDKNTTTQDEIQRISDYCDKFVTLPPTYDDTPYTWTFYHAFFARTVCSTVGYGNISPT 114

Qy    177 TEGGKIFCILYAIFGIPLFGFLLAGIGDQLGTIFGKSIARVEKVFRKKQVS------QTK 230

Db    115 TFAGRMIMIAYSVIGIPVNGLLFAGLGE----YFGRTFEAIYRYRYKKYKMSTDMHYVPPQ 170

Qy    231 IRVISTLF-ILAGCIVFVTIPAVIFKYIEGWTALESIYFVVVTLTTVGFGDFVA--GGN 287
          |: ::|    :|| :| |  |||||||    ||   : ||  |:|||||||||||    :
Db    171 LGLITTVVIALIPGIALFLLPSWVFTYFENWPYSISLYYSYVTTTIGFGDYVPTFGAN 230

Qy    288 AGINYREW--YKPLVWFWILVGLAYFAAVLSMIGDWLRVLSKK----TKEEVGEIKAHA 340
          ||:||:|     | :||||||||:||||||:|||||||:|||        :  | :|
Db    231 QPKEFGGWFVVYQIFVIVWFISLGVLVMMTFIRGLQ-SKKLAYLEQQLSSNLKATQ 288

Qy    341 AEWKANVTABFRETRRRLS------------------VEIHDKLQRAATIRSMERRR----LGL 382
          : :||  |:|  | :                        ::||||  ||:|:||||      |:|
Db    289 NRIWSGVTKDVGYLRMLNELYILKVKPVTDVDIAYTLPRSNSCPDLSMYRVEPAIPS 348

Qy    383 DQRAHSL--DMLSPEKRS--VFAALDTGRFKASSQESINNRP-------------NNLRL 425
          |: :|      ::|: |    :      | :   |   | ||              ||||:
Db    349 RKRAFSVCADMVAAQREAGMVHANSDTELSKLDREKTPETAEAYRQTTDLLAKVVNALAT 408

Qy    426 KGP-----EQLNKHG--QGASEDNI-------------INKFGSTSRLJTKRKNDLKKTLPE-- 467
          |      |  |   |: :                    ::||   |     |:: |::||
Db    409 VKPPPAEQEDAALYGGYHGPSDSQILASEWSFSTVNEPTSPRRPRARACSDFNLEAPRWQ 468

Qy    468 --------------DVQKIYKTFRN------------------YSLDEEKKEETEK 492
                        ||::|:|                      : |  :|  | |
Db    469 SERPLRSSHNEWTWSGDNQQIQEAFNQRYKGQQRANGAANSTMVHLEPDALEEQLKK 525

RESULT 4
T43509
probable potassium channel chain n2P38  - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jan-2000
C;Accession: T43509
R;Wang, Z.W.; Salkoff, L.
submitted to the EMBL Data Library, August 1998
A;Description: Potassium channels in C. elegans.
A;Reference number: Z22450
A;Accession: T43509
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-329 <WAN>
A;Cross-references: EMBL:AF083652; PIDN:AAC32863.1

Query Match             11.4%;  Score 315;  DB 2;  Length 329;
Best Local Similarity   31.6%;  Pred. No. 1.4e-14;
Matches    86;  Conservative   48;  Mismatches   99;  Indels   39;  Gaps    9;

Qy     73 VAIFVVVVVLVTGGLVFRALEQPPESSQKNTIALEKAEFLRDHVCVSPQELETL---- 127
          : :| :|||   |||  |||  ::  |  :            :       ||:
Db      9 LSLIVCTLTYLLVGAAVFDALETENEILQKLVQRVR-EKLKTKYNMSNADYEILEATIV 67

Qy    128 --IQHALDADNAGVSPIGNSSNNSSHWDLGSAFFFAGTVITTIGYGNIAPSTEGGKIFCI 185
            :         ||||:|:|::||||||:||||||||||:||||||||
Db     68 KSVPH-----KAGY---------QWKFSGAFYFATTVITTIGYGHSTPMTDAGKVFCM 111

Qy    186 LYAIFGIPLFGFLLAGIGDLGTIFGKSIARVEKVFRKKQVSQTKIRVISTILFIL---- 241
          |:|  |||||||||||||||||||:|   ||:|  ||:|
Db    112 LYALAGIPLGLIMFQSIGERMNTFAAKLLRFIRRAAGKQPI------VTSSDLIIFCTGW 165

Qy    242 AGCIVFVTIPAVIFKYIEGWTALESIYFVVVTLTTVGFGDFVAGGNAG-INYREWYKPLV 300
          :::|  |  :  |  ::: |  ||  : ||  |:|||||||:||:|| ||:|
Db    166 GGLLIFG--GAFMFSSYENWTYFDAVYYCVTLTTIGFGDYVALQKRGSLQTQPEVFFS 223

Qy    301 WFWILVGLAYFAAVLSMIGDWLRVLSKKTKEE 332
          ||||||||:||||||:|||||||:|||::| |
Db    224 LVFILFGLTVISAAMNLL--VLRFLTMNTEDE 253

RESULT 5
T32347
outward rectifier potassium channel homolog twk-23  - Caenorhabditis elegans
C;Species: Caenorhabditis elegans

C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C;Accession: T32347
R;Murray, J.; Wohldmann, P.; O'Neal, D.
submitted to the EMBL Data Library, September 1997
A;Description: The sequence of C. elegans cosmid F34D6.
A;Reference number: Z21153
A;Accession: T32347
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-336 <MUR>
A;Cross-references: EMBL:AF025454; PIDN:AAC71151.1; GSPDB:GN00020; CESP:F34D6.3
A;Experimental source: strain Bristol N2; clone F34D6
C;Genetics:
A;Gene: twk-23; CESP:F34D6.3
A;Map position: 2
A;Introns: 44/3; 102/1; 136/1; 180/1; 207/1; 265/2; 296/3

Query Match     11.1%;   Score 307;  DB 2;  Length 336;
Best Local Similarity   30.3%;   Pred. No. 5.5e-14;
Matches    84;  Conservative   50;  Mismatches  101;  Indels   42;  Gaps    9;

Qy      73  VAIFVVVVVYLVTGGLVFRALEQPFESSQKNTIALEKAEFLRDHVCVSPQELETLIQHAL 132
                :::  :   :::|  ||  | ||||   :              :::|     ::  :
Db       9  LSLIVCTLTYLLVGAAVFDALETENEILQVRGLG--------------BPRKLVQRVREKL  55

Qy     133  ---DADNAG-------VSPIGNSSNNSSHWDLGSAFFFAGTVITTIGYGNIAPSTEGG 180
                |  :         | :  ||||||||||| ||||| ||||||| |||
Db      56  KTKYNMSNADYEILEATIVKSVPHKA--GYQWKFSGAFYFATTVITTIGYGHSTPMTDAG 113

Qy     181  KIFCCLYAIFGIPLFGFLLAGIGDQLGTIFGKSIARVEKVFRKKQVSQTKIRVISTILFI 240
                |:||||||| |||||||||||||    |:  :       :|  :        |:|  |
Db     114  KVFCMLYALAGIPLGLIMFQSIGERMNTFAAKLLRFIRRAAGKQPI------VTSSDLII 167

Qy     241  L----AGCIVFVTIPAVIFKYIEGWTALESIYFVVTLTTVGFGDFVAGGNAG-INYREW 295
                          ::|   | |:  | |||   |||||||||||| | |||||   :  :
Db     168  FCTGWCGLLIFG--GAFMFSSYENWTYFDAVYYCFVTLTTIGFGDYVALQKRGSSLQTQPE 225

Qy     296  YKPLVWFWILVGLAIFAAVLSMIGDWLRVLSKKTKEE 332
                |  | |  ||| ||  ||  ||||||||||||
Db      226  YVFFSLVFILFGLTVLSAAMNLL--VLRFLTMNTEDE 260

RESULT 6
T43361
probable potassium channel chain n2P20 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 11-Jan-2000
C;Accession: T43361
R;Wang, Z.W.; Salkoff, L.
submitted to the EMBL Data Library, August 1998
A;Description: Potassium channels in C. elegans.
A;Reference number: Z22450
A;Accession: T43361
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-364 <WAN>
A;Cross-references: EMBL:AF083646; PIDN:AAC32857.1

Query Match     10.9%;   Score 300.5;  DB 2;  Length 364;
Best Local Similarity   26.8%;   Pred. No. 1.8e-13;
Matches   106;  Conservative   78;  Mismatches  124;  Indels   87;  Gaps   19;

Qy      70  KTVVAIFVVV--VVYLVTGGLVFRALEQPFESSQKNTIALEKAEFLRDHV----CVSPQE 123
                |:  |  ::::  | ||   ||     |:|| :  |   :
Db       7  KSARALLLILSTFYLLFGAMVFDKLE-----SEKDTWVRDEIERITDRLCHKYNFSERD  61

Qy     124  LETLIQHALDADNAGVSPIGNSSNNSSHWDLGSAFFFAGTVITTIGYGNIAPSTEGGKIF 183
                | :          ||| || ||||||||| ||||| |||||||||||| |
Db      62  L-----HLFEA--IAIKSIPQQA--GYQWQFAGAFYFATTVITTVGYGHSAPSTNAGKLF 112

Qy     184  CILYAIFGIPLFGFLLAGIGDQLGTIFGKSIARVEKVFRK------KQVSQTKIRVIS-T 236
                :::|:||:  :   ||:|  |   ||:|        :        |:|  :|:|  ::|  :
Db     113  CMIFALFGVPMGLIMFQSIGERVNTFIAYSLHKFRDSLHQQGFTCLQEVTPTHLLMVSLT 172

RESULT 7
T25392
hypothetical protein T28A8.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T25392
R;Lloyd, C.
submitted to the EMBL Data Library, March 1997
A;Reference number: Z20027
A;Accession: T25392
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-393 <WIL>
A;Cross-references: EMBL:Z92813; PIDN:CAB07286.1; GSPDB:GN00021; CESP:T28A8.1
A;Experimental source: clone T28A8
C;Genetics:
A;Gene: CESP:T28A8.1
A;Map position: 3
A;Introns: 73/1; 112/3; 179/2; 209/3; 287/2; 310/3; 364/2

Query Match     10.8%;   Score 298.5;  DB 2;  Length 393;
Best Local Similarity   27.1%;   Pred. No. 2.7e-13;
Matches    85;  Conservative   50;  Mismatches   94;  Indels   85;  Gaps   11;

Qy      69  WKTV-------VAIFVVVVYLVTGGLVFRALEQPFESSQKNTIALEKAEFLRDHVCVSP 121
                |||              :|||| ||||| :  ||  |     |  ::
Db       4  WKTYARIILAHVSLIVLSVVYVGFGAFLFYQLEQP-----NEVEVRARNIERFNI---- 53

Qy     122  QELETLIQHALDADNAGVSP------------------------IG----NSSNNS 149
                :|:         | : ::                         ||    ||||||
Db      54  -HKRQMIEHLWEMRESGIGQHVEVEDLAVKVVDNVTRILFEAFDTHCIGAKHLRPGGEDED 112

Qy     150  SHWDLGSAFFFAGTVITTIGYGNIAPSTEGGKIPCILYAIFGIPLFGFLLAGIGDQLGTI 209
                ||| ||||| |||||||| |||||| :  :  | |||| ||||| |||| :  :
Db     113  YNWTYWTALFFTTLLTTIGYGNLTPVTGRGKLLCILYALFGVPL---ILITVAD-IGKF 168

Qy     210  FGKSIARVEVFRK--KQVSQTKIRVIST------------------------ILFILAGCI 245
                |||:  :  |  :  |:|  :|:|:|                         ||| |
Db      169  LSENIVQLYTWYRKLREKCSKQKYSVISSKDDKNKEGDLNLDHLENYISIPIFLIVAILL 228

Qy     246  VFVTIPAVIFKYIEGWTALESIYFVVTLTTVGFGDFVAGGNAGINYREWYKPLVWFWIL 305
                ::|:  :|       ||||  ||||||| |||||    :    |:
Db      229  SYITFGAVVLSMWEGWDFFSGFYFSFIMMTTVGFGDIVP-----LKRBYY-ILDLCYII 281

Qy     306  VGLAYFAAVLSMIG 319
                :|:|  |:: :||
Db      282  IGLSTTMCIDLVG 295

RESULT 8
H88124
protein T12C9.3 [imported] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
C;Accession: H88124

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Qy     237  ILF--ILAGCIVFVTIPAVIFKYIEGWTALESIYFVVTLTTVGFGDFVAGGNAGINYRE 294
                |||  :|  | |:|       ||  :: :::    ::|||||||||||||
Db      173  IGFMVIVSGTYMFHT-------IEKWSIFDAYYFCMITFSTIGFGDLVP--LQQVNALQ 222

Qy     295  WYKPLVWF---WILVGLAYFAAVLSMIGDWLRVLSKKTKEVGEIKAHAAEWKANVTAE 350
                :||||||      ||| |::  ::    :::   ||       |:|:|     |::|
Db      223  -DQPLYVFATIMFLLIGLAVFSACVNLL-------------VLGFMASNADE---VTAA 264

Qy     351  FRE--------TRRRLSVEIHDKLQRAATIRSMERRRIGLDQRAHSLDMLS------ 393
                :            |:  : : :: :: ||  |: |    :|:    :  ||
Db      265  QREPPSAIVLERFTRNSLVDSQIFNIQKHSTVGVLP----GRPPRMYSIVPNSTADVHLR 320

Qy     394  -PEKRSVFAALDTGRFKASSQE---SINNRPNNL 423
                : :   :     : :|: | :      :||:|||
Db      321  RRSTRRSIQDTVCCGCFKPRPPRHRFSLTRRPTNI 355

R:anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A:Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog
A:Reference number: A75000; MUID:99069613; PMID:9851916
A:Note: see websites genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/Projects/C_ele
A:Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
A:Accession: H88124
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1910 <STO>
A:Cross-references: GB:chr_II; PIDN:AC71141.1; PID:g1086770; GSPDB:GN00020; CESP:T12C9.3
A:Note: proline-rich
C;Genetics:
A;Gene: T12C9.3
A;Map position: 2

Query Match             10.8%;   Score 298.5;  DB 2;   Length 1910;
Best Local Similarity   21.2%;   Pred. No. 2.2e-12;
Matches   121;  Conservative  90;  Mismatches  90;  Indels  163;  Gaps  22;

```
Qy     10  LSLVAVPAAAPVCQPKSATNGQPPAP-APTP---TPRLSISSRATVVARWEGTSQQGLQT  65
               :  ||  :| :::    |   ::||  |:: |      |:|  | ||
Db    134  LSFSTSPATRKACLSKQV--HPPIPHHPTPQFSRRFSIPPGLLESARPDDETTTLQN  190

Qy     66  VMKWKTV---VAIFVVVVYLVTGGLVFRALEQPFESSQK---NTIALEKA-------  110
               ||:|       | :||  :| ::|  | :| |     :|  :
Db    191  IRKYAKLALPHIVLVLVVCVCIYATIGAWIFYTLESPNEDRLKETGRKTIAEMRSNLIYKIN  250

Qy    111  -------EFLRDHVCVSPQEL-----ETLIQHA---------LDDANAGVSPIGN  144
                     |  | :  ::   |     :|:|            || |  |||
Db    251  NNEKEVWKEDIEKELMLYSEKLYKAFKEQYVRYSDVRTIGFEGRSSYEEADETG----GD  306

Qy    145  SSNNSSH-------------WDLGSAFFAGTVITTIGYGNIAPSTEGGKIFCILYAIF  190
               ::|:|:             | |||||||||| |||:  || : || :|| : :|
Db    307  SERKRRHRGNKRGDRGSEKMWTTSALFFAATTMATIGYGNIVPVTPLGLACVLFALF  366

Qy    191  GIPLFGFLLAGIGDQLG--TIF----GKSIARVEKVFRK--------------------  223
               | |||||||| |||   |:|    |:||||:||  |
Db    367  GAPIAIITIGDLGKFLSECTIWLYKHMRKGSARLDSAWKPRGLEDSISDDLESASKNQD  426

Qy    224  -------------KQVSQTKIRVISTLFILAGCIVFVTIPAVIFKYIEGWTALESIYFVVVTLT  275
                            ||||||||| ||| |: |:|  || ||||:||||| :||::||| | |
Db    427  SSILDMDMDEIDKSEVPVLMVFTIIL---LYIAFGGILFSILEDWSYMDAFYYSFISLT  482

Qy    276  TVGFGDFVAGNAGINYREWYKPLVWFWILVGLAYFAAVLSMIG------------319
               :||||| :|||||| |:| ||:|   |:|  :|  |  |
Db    483  TIGFGDIVPENHD------YIAIMLIYLGVGLSVTTMCIDLAGIQYIQIKIHYFGRKFQG  535

Qy    320  -DWLRVLSKKTK----------EEVGEIKAHAAEWKANVTAEFRETRRRLSVEIHDKLQR  368
                | |:|: |:|          ||  ||||||  | | | | || || ::  :
Db    536  TDLLQYLKKKRMLERRLAMGQQEBILRKYVHAVE-------KFEREQEQLQQKMEEDPP  588

Qy    369  AATIRSMERRRLGLDQRAHSL-------------DMLSPEKRSV--FAALDTGRFKASSQES  415
               |:   : : :|  :| | |            |:| | | |    | | ||  | |:|:|
Db    589  SIESKGFDNSMMRIDDSLSAFQLRFYDTYDEEDLFSPTIHSVRSFQPSVWSHSSARSQSF  648

Qy    416  I---NNRPNNLRLKGPBQLNKHGQGASEDNI  443
               :      ::| :|:  :| : :
Db    649  CRFQRNRGASWDESGP-SLSEHCSLSTEPSV  678
```

RESULT 9
T19860
hypothetical protein C40C9.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
C;Accession: T19860
R;Hembry, C.
submitted to the EMBL Data Library, March 1996
A;Reference number: Z19188
A;Accession: T19860
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA

A;Residues: 1-334 <WIL>
A;Cross-references: EMBL:Z70266; PIDN:CAA94204.1; GSPDB:GN00028; CESP:C40C9.1
A;Experimental source: clone C40C9
C;Genetics:
A;Gene: CESP:C40C9.1
A;Map position: X
A;Introns: 34/1; 60/2; 98/1; 145/3; 160/3; 181/1; 204/1; 252/2; 279/2; 306/3

Query Match             10.5%;   Score 290.5;  DB 2;   Length 334;
Best Local Similarity   28.6%;   Pred. No. 7.8e-13;
Matches   89;  Conservative  67;  Mismatches  94;  Indels  61;  Gaps  15;

```
Qy     70  KTVVAIFVVV--VVYLVTGGLVFRALEQPFESSQKNTIALEKAEFLRDHV-----CVSPQE  123
               | :| ::    : ::: ||  |     :|  ::| |:  :|| | :::
Db      7  KSARALLLILSTFTYLLFGAMVFDKLE-----SEKDTWVRDEIRITDRLKHKYNFSERD  61

Qy    124  LETLIQHALDADNAGVSPIGNSSNNSSHWDLGSAFFAGTVITTIGYGNIAPSTEGGKIF  183
               |  :|  |  |  ||  |        |:  ::| | ||| ::||:||  | :||
Db     62  L-----HLFEA--IAIKSIPQQA--GYQWQFAGAFYFATVITTVYGYGHSAPSTNAGKLF  112

Qy    184  CILYAIFGIPLFGFLLAGIGDQLGTIFGKSIARVEKVFRK------KQVSQTKIRVIS-T  236
               | ||:||| ||| |::  ||  ::::|  :: || | |        ||||||||||| |
Db    113  CMIFALFGVPMGLIMFQSIGERVNTFIAYSLHKFRDSLHQQGFTCLQEVTPTHLLMVSLT  172

Qy    237  ILF--ILAGCIVFVTIPAVIFKYIEGWTALESIYFVVVTLTTVGFGDFVAGGNAGINYRE  294
               | |   | |  :|  ||    ||:  |    |:  : ||:|| ||| |:   ||| | |
Db    173  IGFMVIVSGTYMFHT-------IEKWSIFDAYYFCMIFSTIGFGDLVP--LQQVNALQ  222

Qy    295  WYKPLVWF---WIIVGLAYFAAVLSMIGDWLRVLSKKTKEEVGEIKAHAAEWKANVTAE  350
               ||| | |    |: || |  | :      | :     | |
Db    223  -DQPLVFATIMFILJGLAVFSACVNLL---------------VLGFMASNADE----VTAA  264

Qy    351  FRETRRRLSVE  361
               :
Db    265  QREPPSAIVLE  275
```

RESULT 10
T45032
hypothetical protein Y39B6B.f [imported] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jul-2000
C;Accession: T45032
R;Wilson, R.; Ainscough, R.; Anderson, K.; Baynes, C.; Berks, M.; Bonfield, J.; Burton, J
raser, A.; Fulton, L.; Gardner, A.; Green, P.; Hawkins, T.; Hillier, L.; Jier, M.; Johnst
B.; O'Callaghan, M.; Parsons, J.; Percy, C.; Rifken, L.; Roopra, A.; Saunders, D.
Nature 368, 32-38, 1994
A;Authors: Shownkeen, R.; Sims, M.; Smaldon, N.; Smith, A.; Smith, M.; Sonnhammer, E.; St
tock, L.; Wilkinson-Sproat, J.; Wohldman, P.
A;Title: 2.2 Mb of contiguous nucleotide sequence from chromosome III of C. elegans.
A;Reference number: S43531; MUID:94150718; PMID:7906398
A;Accession: T45032
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-392 <WIL>
A;Cross-references: EMBL:AL132896; NID:g6434440; PIDN:CAB60911.1; PID:g6434446
A;Experimental source: clone Y39B6B
C;Genetics:
A;Map position: 3
A;Introns: 47/2; 82/2; 106/3; 151/1; 220/1; 260/3; 370/3
A;Note: Y39B6B.f

Query Match             10.2%;   Score 282.5;  DB 2;   Length 392;
Best Local Similarity   31.7%;   Pred. No. 3.5e-12;
Matches   77;  Conservative  46;  Mismatches  97;  Indels  23;  Gaps  8;

```
Qy     90  FRALEQPFESSQKNTIALEKAEFLRDHVC---VSPQELETLIQHALDADNAGVSPIGNSS  146
               |||:|| ||:| :||||| | |  : |    |: |||:|| | | | || | | ::
Db    118  FSRIEYPLEKIEREAY-LDYQNQWRDRLIQLDIDESEIDKLF---LNIREAALNGIWMDR  173

Qy    147  NNSS--HWDLGSAFFFAGTVITTIGYGNIAPSTEGGKIFCILYAIFGIPLFGFLLAGIGD  204
               ||:    | |||| || |||::|||||   | |||||| || :  |: ||| |::
Db    174  NLTSDPNWTFGQAFFFAGTLISTVGYGRVSPRTEYGKLFTILYCVIGIPLTLALLSAIVA  233
```

```
Qy   205 QL----GTIFGKSIARVEKVFRKKQVSQTKIRVI--STILFILAGCIVFVTIPAVIFKYI 258
          ::    |::                          |   |||   |||
Db   234 RMREPSHKLRGLLNQRLGHLFTVNHIQLIHVGVVFASLLLFVFA------IPAWVFSSI 286

Qy   259 E-GWTALESIYFVVVTLTTVGFGDFVAGGNAGINYREWYKPLVWFWILVGLAYFAAVLSM 317
          : |  |     :  :||||| |||            :     | |    |
Db   287 ETDWSYLDAFYYCFVSLTTIGLGDFEPGDPNQSFRGLYKIGATYLMGGLCCMMLFLAT 346

Qy   318 IGD 320
          |
Db   347 LYD 349
```

RESULT 11
T24265
hypothetical protein T01B4.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
R;Wilkinson, J.
submitted to the EMBL Data Library, March 1996
A;Reference number: Z19866
A;Accession: T24265
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-522 <WIL>
A;Cross-references: EMBL;Z70036; PIDN;CAA93875.1; GSPDB;GN00028; CESP:T01B4
A;Experimental source: clone T01B4
C;Genetics:
A;Gene: CESP:T01B4.1
A;Map position: X
A;Introns: 95/3; 142/1; 224/3; 290/1; 458/1

```
Query Match             9.7%;  Score 268.5;  DB 2;  Length 522;
Best Local Similarity  22.3%;  Pred. No. 4.9e-11;
Matches  120;  Conservative   89;  Mismatches 181;  Indels 147;  Gaps  21;

Qy    73 VAIFVVVVVYLVTGGLVFRALE--QPFE-------SSQKNTIALEKAEFLRDHCVSP 121
          :   :       | |: :|:|    ::         ||:  |       |::
Db    39 IMLILILGYACLGGYMFQALEYDQQOLELEAEKRVRLSESSLLAVNLLEHLKQMNCGQS  98

Qy   122 QE-------LETLIQHALDADNAGVSPIGNSSNNSSHWDLGSAFFAGTVITTIGYGNIA 174
          ::        : :                     |  |:  :|||::|||||||||||
Db    99 NEKRCLELITKFIQRSDEERGEG---------WRWDFWNSVFFSATIFTTIGYGNLA 147

Qy   175 PSTEGGKIFCILYAIFGIPLFGFLLAGIGDQLGTIFGKSI-----ARVEKVFRKKQVSQT 229
          |:  | || ::||:|:|||| ||:| || |           :     |:  |  :::
Db   148 CKTNLGRIATIIYGMIGIPLMLFVLKNFG-ELCVKWAKKIQPNVQQCLKKCFGRKQKRAS 206

Qy   230 KIRVIST----------ILFILAGCIVFVTIPAVIFKYIEGWTALESIY 268
          |:                |  |: :||:||| ||   |    ||  ||
Db   207 SLASITSKEMLEVFFEVPEDDKEDTTFQLRWGLLIVLFVVLCSFVVSFWENWDFITAFY 266

Qy   269 FVVVTLTTVGFGDFVAGGNAGINYREWYKPLVWFWIL--VGLAYFAAVLSMIGD------ 320
          | :::||||||||:|:          |     | |    ||| |:|:|
Db   267 FFFVSLSTIGFGDIVP--------DHPRTACALFVLYFIGLALFAMVYAILQERVENQY 317

Qy   321 -W-LRVLSKKTKEEVGEIKAHAAEWKA--NVTAEFRETRRRLSVEIHDKLQRAATIRSM 375
          |  | :|                 :|    |:  || |||||:|: |||  |   ::|
Db   318 MWALELIDQKYQEKLKQDMYDEDEKKADKDMHFSKKEPVRGPRILLQD-LLRGPDLKIS 376

Qy   376 ERRRLGLDQRAHSLDMLSPEKRSVFAALDTGRFKASSQESINNRPNNLRLKGP-EQLNKH 434
          ::|                          |     |      ||      :    :
Db   377 GGRRSSSD--ASSVITEASDE------DTRHFKV---------GRAILAEFAPDERASNH 420

Qy   435 GQGASEDNIINKFGSTSRLTKRKNKDLKKTLPEDVQKIYKTFR--------NYSLDEEK 485
          |                                       :        :||:|:
Db   421 GTQLNSCTVSNEHDSC--------------QIEAIVFSPHFISFINFQFNYSSDESL 463

Qy   486 KEETEKMCNS------------DNSSTAM------LTDCIQQHAELENG 517
          :|||::|||             ||:||:       |||::           |
Db   464 EEHQLETYDTSGTPPPYGDPTPTNFQTRDETVTSLAEKTPLSLNKVLEEENEDENG 520
```

RESULT 12
T21834
hypothetical protein F36A2.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T21834
R;Lennard, N.
submitted to the EMBL Data Library, October 1996
A;Reference number: Z19476
A;Accession: Z19476
A;Accession: T21834
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-528 <WIL>
A;Cross-references: EMBL;Z81077; PIDN;CAB03071.1; GSPDB;GN00019; CESP:F36A2.4
A;Experimental source: clone F36A2
C;Genetics:
A;Gene: CESP:F36A2.4
A;Map position: 1
A;Introns: 45/3; 81/3; 114/3; 151/3; 195/1; 306/1; 326/1; 368/2; 413/1; 464/2; 494/1

```
Query Match             9.6%;  Score 265.5;  DB 2;  Length 528;
Best Local Similarity  22.2%;  Pred. No. 8e-11;
Matches  122;  Conservative   86;  Mismatches 163;  Indels 179;  Gaps  26;

Qy    79 VVVYLVTGGLVFRALE------QPFE------SSQKNTIALEKA 110
          :: :   |:: |:::|                |||
Db    25 VVLYIILGAIVFQMLEGEHLDNFSDFNPKKCHFGPKMVDKFFETIFRRWSKGAN--FKKS  81

Qy   111 EFLRDHCVSPQ-----------ELETLI---QHALDADNAGVSPI--- 142
          :|:                      :
Db    82 ALKKDHMAKIEQNAKDYDVDKLWSVAKRDRDKYKNVEDLIKSVKEDTVDDFNDYVDTVFYA 141

Qy   143 ------GNSSNNSSHWDLGSAFFAGTVITTIGYGNIAPSTEGGKIFCILYAIFGIPLFGF 197
                :|:||||| :|||   ||||||:::|
Db   142 HRAVRHGYDEDSPTWDFANSVFFTTMLTSIGYGVVAPSTFGGRLFGVIVICLIGIPLTLV 201

Qy   198 LLAGIGDQLG-TIF------GKSIARVEKVFRKKQVSQ-------TKIR 232
          ::     |  |                  |:
Db   202 TVANVAKFLSETIFFLHYELWNKCLEWKRK--RKGEVEADPLQPMFGDDENEEEILDRVR 259

Qy   233 VIS-----TILFILAGCIVFVTIPAVIFKYIEGWTALESIYFVVVTLTTVGFGDF-VAGGN 287
          :::       |  |: :||:||||||||||| ::|:| :|: :|||||| :|||
Db   260 LVRFPPLTVFFFV---FVYGCIAAWVVRYWETWTYVESLYFIFISILTVGFGDIRPSPGN 316

Qy   288 AGINYREWYKPLVWF--WILVGLAYFAAVLSMIGDW----LRVLSKKTKEE------VGE 335
          |||||||||||:||      |||||| ::::|        | |:| | ||      |:
Db   317 -----------------IWVTLAFVVVGVILTTMCMDVVGRMYLKEIHYLGRKLKSSNPFYLLRE 364

Qy   336 IKAHAAEWKANVTABFRETRRRLSV-------------EIHDKLQRAATIRSMERRRL 380
          |: |||| ||   ||  |  |::              :::
Db   365 AKAR-----RRRAAMASLLAQLAKGMIFAHKDYNELARKKSKRKEKRR- 408

Qy   381 GLDQRAHSLDMLSPEKRSVFAALDTGRFKASSQESINNRPNNLRLKGPEQLNKHGQGASE 440
          :| | ::|| |: | ||||:||::|||||||:::|||||||||||||
Db   409 --GSHVL----PNEKFMFARLPPD--PFSDCQVSTSAYSVRLAWAPPF------SP 451

Qy   441 D----NIINKFGSTSRLTKRKNKDLKKTLPEDVQKIYKTFRNYSLDEKKEETEKMC- 494
          |              ||  |:::   |::|
Db   452 DPDLTYNIRYLRNATAVFKDGQRSPLSRALFIKTDKI-EFHKGHCVGHSKTIDVMDSICE 509

Qy   495 NSDNSSTAML 504
          |:||::|||
Db   510 KEDNETTALL 519
```

RESULT 13
T26229
hypothetical protein W06D12.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T26229

```
R;Basham, V.
submitted to the EMBL Data Library, November 1996
A;Reference number: Z20177
A;Accession: T26229
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-444 <WIL>
A;Cross-references: EMBL:Z82073; PIDN:CAB04923.1; GSPDB:GN00023; CESP:W06D12.2
A;Experimental source: clone W06D12
C;Genetics:
A;Gene: CESP:W06D12.2
A;Map position: 5
A;Introns: 70/3; 127/1; 170/1; 197/3; 326/1; 405/3

Query Match          9.6%;    Score 264.5; DB 2;  Length 444;
Best Local Similarity 20.3%;  Pred. No. 7.5e-11;
Matches  103;  Conservative  80;  Mismatches 170;  Indels 155;  Gaps 16;

Qy   78 VVVYLVTGGLVFRALEQPFESSQKNTIALEKAEFLRDHVCV------------------S 120
        ::|:|||
Db   23 VLIVYSFLGAGLFVLCEAENEKSLKHE--DNMRVLRTSIAAKQVFVQRLQNMYSGNGSS 79

Qy  121 PQELETLIQHALDADNAGVSPIGNSSNNSSHWDLGSAFFFAGTVITTIGYGNIAPSTEGG 180
Db   80 SEFSETKLRRVLSEYDAAMG-ISIDSKMKTRWDIWGGLYYAGTIYTTIGYGDLAAETIWG 138

Qy  181 KIFCILYAIFGIPLFGFLLAGIGDQLGTI---FGKSIARV------EKVFRKK------- 224
Db  139 RICTMLYAMIGIPIVINLNDWGNMLFYFVDHFWQNIGRQWIQSLRQKLRRRKVQSLEEG 198

Qy  225 ---------QVSQTK-----IRVISTILFILAGCIVFVTIPAVIFKYIEGWT 262
Db  199 SIDKTPLMETSSTPPSPQNPNGTRPIPLLLVLIVLFFWMIQCVAY------FAYFENWT 251

Qy  263 ALESIYFVVVTLTTVGFDFVAGGNAGINYREWYKPLVWFWILVGLAYFAAVLSMIGDWL 322
Db  252 LFESVYFFISMTTIGFGDFTPSHTVAVG----------GIVFILGGLSLVSMCI 296

Qy  323 RVLSKKTKEEVGEIKAHAAEWKANVTAEFRETRRRLSVEIHDKLQRAATIRSMERRRLGL 382
Db  297 NVI-------------CMQLEFIFNQIVQRIENDFKNTLSVAA--EESRKKSIGV 336

Qy  383 DQRAHSLDMLSPEKRSVFAALDTGRFKASSQESINNRPNNLRLKGPEQLNKHGQGASEDN 442
Db  337 -------------SEFGSIDPSKKK-----TMRTDG----------------N 355

Qy  443 IINKFGSTSRLTKRNKDLKKTLPEDVQKIYKTFRNYSLDEEKKEETEKMCNSDNSSTA 502
Db  356 VAEKYSENMEM---GNKLLMRFMSNHQKKML---------NEKFDERAKMRNSGTQTTS 402

Qy  503 MLTDCIQQHAELENGMIPTDTKDREPEN 530
Db  403 QIKVASVQTAERYEQTWDEDPEEEQPKS 430

RESULT 14
T16426
hypothetical protein F52E4.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 18-Feb-2000
R;Martin, J.
submitted to the EMBL Data Library, April 1996
A;Description: The sequence of C. elegans cosmid F52E4.
A;Reference number: Z18512
A;Accession: T16426
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-551 <MAR>
A;Cross-references: EMBL:U56964; NID:g1293826; PID:g2078439; PIDN:AAB54033.1; GSPDB:GN00
A;Experimental source: strain Bristol N2; clone F52E4
C;Genetics:
A;Gene: CESP:F52E4.4
```

```
A;Map position: X
A;Introns: 14/3; 65/3; 95/2; 118/1; 165/3; 267/1; 297/2; 334/3; 385/2; 477/1; 513/2

Query Match          9.6%;    Score 264; DB 2;  Length 551;
Best Local Similarity 20.3%;  Pred. No. 1.1e-10;
Matches  108;  Conservative  94;  Mismatches 205;  Indels 124;  Gaps 16;

Qy   74 AIFVVVVLVTGGLVFRALEQPFESSQKNTIALEKAEFLRDHVCVSPQELETL------ 127
        ::|:|||:|
Db   24 SLLMVLLYSFLGGFIFDRIETNAHAEMK------RNERINRTACVS-QILHSIHRWSHN 76

Qy  128 ---IQHALDADNAGVSPIGNSSNNSSHWDLGSAFFFAGTVITTIGYGNIAPSTEGGKIF 183
Db   77 QTHKVQYAEDIADC---FEPEKDERSEWNFVTATLYGFGIVTTLGYNRIAPITYTGRMF 132

Qy  184 CILYAIFGIPLFGFLLAGIGDQLGTIFGKSIARVEKVFRRKQVSQTKI------RVIS 235
Db  133 CIVYIGICGIPVTMIIIANVGQYLNNFAGDSRRKIEAYRQQRRMSKASLAGKIYKESSIQV 192

Qy  236 TLFILAGCIVFVTIPAVIFKYIEG-WTALESIYFVVVTLTTVGFDFVAGGNAGINYRE 294
Db  193 TSLALLCVFLIYVAVGALLLPLLNGELDFFNGLYFNFLCLTAIDFGQLVP-----IRV 245

Qy  295 WYKPLVWFWILVGLA--------------------------YFAAVLSMIGDWLR 323
Db  246 ELLPITFLYVCIGLAITTIAINIGSEYMKKLLHYWGKKMKNAAQTRIWFGGKTLKVRDLLH 305

Qy  324 VLSKKTKEEVGEIKAHAAEWKANVTAEFRETRRRLSVEIHDKLQRAATIRSM------- 375
Db  306 AVGKKCGVEPGMIDALDLENVVERTIAMQEGREP-PEDLNDEPPREPSPRSIIHSPCSTR 364

Qy  376 ------------------ERRRLGLDQRAHSLDMLSPEKRSVFAALDTGRFKASS 412
Db  365 PSNPMSPPSPREDHPFIFKMDAPAPRSPLPLPAYELDI---KKPIFQALSNEFMNQSA 420

Qy  413 QESINNRPNNLRLK-GPEQLNKH-----------GQGASEDNII------NKFGSTSRLTKR 456
Db  421 QEKLFNDLDTFQIEINTELLVEDHKCESVIIIEPPATFEDMTIQHSLCVEDYEREKVPKR 480

Qy  457 KNKDLKKTLPEDVQKIYKTFRNYSLDEEKKEETEKMCNSDNSSTAMLTDC 507
Db  481 -FREKKEMYGRDPRKLYET---YQEEWDRLERLSRDKHGPRRKSVLNLSNC 527

RESULT 15
T43357
potassium channel chain n2P16 homolog - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 11-Jan-2000
C;Accession: T43357
R;Wang, Z.W.; Kunkel, M.T.; Wei, A.; Butler, A.; Salkoff, L.
Ann. N. Y. Acad. Sci. 868, 286-303, 1999
A;Title: Genomic organization of nematode 4TM K+ channels.
A;Reference number: Z22446; MUID:99342707; PMID:10414302
A;Accession: T43357
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-555 <WAN>
A;Cross-references: EMBL:AF083645; PIDN:AAC32856.1

Query Match          9.6%;    Score 264; DB 2;  Length 555;
Best Local Similarity 20.3%;  Pred. No. 1.1e-10;
Matches  108;  Conservative  94;  Mismatches 205;  Indels 124;  Gaps 16;

Qy   74 AIFVVVVLVTGGLVFRALEQPFESSQKNTIALEKAEFLRDHVCVSPQELETL------ 127
        ::|:|||:|
Db   28 SLLMVLLYSFLGGFIFDRIETNAHAEMK------RNERINRTACVS-QILHSIHRWSHN 80

Qy  128 ---IQHALDADNAGVSPIGNSSNNSSHWDLGSAFFFAGTVITTIGYGNIAPSTEGGKIF 183
Db   81 QTHKVQYAEDIADC---FEPEKDERSEWNFVTATLYGFGIVTTLGYNRIAPITYTGRMF 136

Qy  184 CILYAIFGIPLFGFLLAGIGDQLGTIFGKSIARVEKVFRRKQVSQTKI------RVIS 235
```

```
Db       |||:|  |||::  ::|:::|:    |:|    :::|:  :
     137 CIVYGICGIPVTMIIIANVGQYLNFAGDSRRKIEAYRQQRRMSKASLAGKIYKESSIQV 196

Qy       |::|  :  :||  :  |: :   ::|:   :  |  :
     236 TILFILAGCIVFVTIPAVIFKYIEG-WTALESIYPVVVTLTTVGFGDFVAGGNAGINYRE 294
Db       |::|  :  :||  :  |: :   ::|:   :  |  :
     197 TSLALLCVFLIYVAVGALLLPLLNGELDFFNGLYFNFLCLTAIDFGQLVP------IRV 249

Qy       |:  |
     295 WYKPLVWFWILVGLA--------------------------YPAAVLSMIGDWLR 323
Db       |:  : :||:|| |
     250 ELLPITFLYVCIGLAITTAINIGSEYMKKLHYWGKKMKNAAQTRIWFGGKTLKVRDLLH 309

Qy         |  :  |:  |:||:   :|
     324 VLSKKTKEEVGEIKAHAAEWKANVTAEFRETRRRLSVEIHDKLQRAATIRSM------ 375
Db         |  :  |:  |:||:   :|
     310 AVGKKCGVEPGMIDALDLENVVERTIAMQEGREP-PEDLNDEPPREPSPRSIIHSPCSTR 368

Qy.      ---------------ERRRLGLDQRAHSLDMLSPEKRSVFAALDTGRFKASS 412
Db             |  ::| |:  |:  ||
     369 PSNPPMSPPSPREDHPFIFKMDAPAPRSPLPLPAYELDI----KKPIFQALSNEFMNQSA 424

Qy       |||  :  ::|  |          :||: :   :|::|  |
     413 QESINNRPNNLRLK-GPEQLNKH---------GQGASEDNII------NKFGSTSRLTKR 456
Db       |||  :  ::|  |          :||: :   :|::|  |
     425 QEKLFNDLDTFQIEINTELVEDHKCESVIIEPPATFEDMTIQHSLCVEDYEREKVPKR 484

Qy       ::  || |:||:|                  | :::|:| |:::|
     457 KNKDLKKTLPEDVQKIYKTFRNYSLDEEKKEEETEKMCNSDNSSTAMLTDC 507
Db       ::  || |:||:|                  | :::|:| |:::|
     485 -FREKKEMYGRDPRKLYET--YQEWDRLERLSDRKHGPRRKSVLNLSNC 531
```

Search completed: June 29, 2004, 18:19:57
Job time : 23 secs

```
                    GenCore version 5.1.6
          Copyright (c) 1993 - 2004  Compugen Ltd.

OM protein - protein search, using sw model

Run on:   June 29, 2004, 18:12:17 ; Search time 45 Seconds
                                     (without alignments)
                         3772.195 Million cell updates/sec

Title:           US-09-892-360-2
Perfect score:   2760
Sequence:        1 MFFLYTDFFLSLVAVPAAAP.........IPTDTKDREPENNSLLEDRN 538

Scoring table:   BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched:        1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters:   1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   SPTREMBL_25:*
             1:  sp_archea:*
             2:  sp_bacteria:*
             3:  sp_fungi:*
             4:  sp_human:*
             5:  sp_invertebrate:*
             6:  sp_mammal:*
             7:  sp_mhc:*
             8:  sp_organelle:*
             9:  sp_phage:*
             10: sp_plant:*
             11: sp_rodent:*
             12: sp_virus:*
             13: sp_vertebrate:*
             14: sp_unclassified:*
             15: sp_rvirus:*
             16: sp_bacteriap:*
             17: sp_archeap:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query Match | Query Length | DB | ID | Description |
|---|---|---|---|---|---|---|
| 1 | 2578.5 | 93.4 | 535 | 11 | Q8BUW1 | Q8buw1 mus musculu |
| 2 | 2180.5 | 79.0 | 453 | 11 | Q8BZB0 | Q8bzb0 mus musculu |
| 3 | 1247.5 | 45.2 | 426 | 11 | Q920B6 | Q920b6 rattus norv |
| 4 | 1244.5 | 45.1 | 411 | 6 | Q8HY88 | Q8hy88 bos taurus |
| 5 | 1242.5 | 45.0 | 411 | 4 | Q9NRT2 | Q9nrt2 homo sapien |
| 6 | 983.5 | 35.6 | 241 | 11 | Q9CX88 | Q9cx88 mus musculu |
| 7 | 930 | 33.7 | 193 | 11 | Q8BWJ6 | Q8bwj6 mus musculu |
| 8 | 778 | 28.2 | 397 | 11 | Q92414 | Q92414 rattus norv |
| 9 | 478.5 | 17.3 | 502 | 11 | Q9JK62 | Q9jk62 mus musculu |
| 10 | 454 | 16.4 | 257 | 11 | Q80XE0 | Q80xe0 mus musculu |
| 11 | 447 | 16.2 | 184 | 4 | Q8N4V5 | Q8n4v5 homo sapien |
| 12 | 424.5 | 15.4 | 341 | 6 | Q8HZT2 | Q8hzt2 bos taurus |
| 13 | 403 | 14.6 | 307 | 13 | Q801T4 | Q801t4 xenopus lae |
| 14 | 400 | 14.5 | 336 | 11 | Q9ZZT2 | Q9zzt2 rattus norv |
| 15 | 398 | 14.4 | 336 | 11 | Q8R454 | Q8r454 cavia porce |
| 16 | 395.5 | 14.3 | 336 | 11 | Q99L99 | Q99199 mus musculu |
| 17 | 382 | 13.8 | 259 | 6 | O02821 | O02821 oryctolagus |
| 18 | 360 | 13.0 | 331 | 13 | Q8AVI5 | Q8avi5 xenopus lae |
| 19 | 351.5 | 12.7 | 299 | 11 | Q90X34 | Q90x34 mus musculu |
| 20 | 349 | 12.6 | 396 | 11 | Q923V6 | Q923v6 rattus norv |
| 21 | 346.5 | 12.6 | 311 | 11 | Q8B222 | Q8bz22 mus musculu |
| 22 | 345.5 | 12.5 | 395 | 11 | Q9ERU5 | Q9eru5 rattus norv |
| 23 | 345.5 | 12.5 | 312 | 11 | Q9JLD4 | Q9jld4 rattus norv |
| 24 | 327.5 | 11.9 | 312 | 11 | Q8R453 | Q8r453 cavia porce |
| 25 | 315.5 | 11.4 | 329 | 5 | O17185 | O17185 caenorhabdi |
| 26 | 314.5 | 11.4 | 319 | 5 | Q9NEV3 | Q9nev3 caenorhabdi |
| 27 | 312 | 11.3 | 343 | 11 | Q9JU14 | Q9jj14 mus musculu |
| 28 | 311 | 11.3 | 392 | 11 | Q9ESM5 | Q9esm5 rattus norv |
| 29 | 309 | 11.2 | 398 | 5 | Q9VFS9 | Q9vfs9 drosophila |
| 30 | 300.5 | 10.9 | 364 | 5 | O76790 | O76790 caenorhabdi |
| 31 | 298.5 | 10.8 | 393 | 5 | Q9XU07 | Q9xu07 caenorhabdi |
| 32 | 292.5 | 10.6 | 385 | 5 | Q9VYY5 | Q9vyy5 drosophila |
| 33 | 292 | 10.6 | 340 | 5 | Q9VHE0 | Q9vhe0 drosophila |
| 34 | 281 | 10.2 | 426 | 5 | Q816M6 | Q816m6 aplysia cal |
| 35 | 279 | 10.1 | 314 | 11 | Q8QZZ6 | Q8qzz6 cavia porce |
| 36 | 276 | 10.0 | 498 | 5 | Q22940 | Q22940 caenorhabdi |
| 37 | 271.5 | 9.8 | 372 | 5 | Q7YWY7 | Q7ywy7 caenorhabdi |
| 38 | 268.5 | 9.7 | 522 | 5 | Q22042 | Q22042 caenorhabdi |
| 39 | 264.5 | 9.6 | 444 | 5 | O45891 | O45891 caenorhabdi |
| 40 | 264 | 9.6 | 555 | 5 | Q20673 | Q20673 caenorhabdi |
| 41 | 262.5 | 9.5 | 572 | 5 | O45422 | O45422 caenorhabdi |
| 42 | 261 | 9.5 | 618 | 5 | P90863 | P90863 caenorhabdi |
| 43 | 260 | 9.4 | 461 | 5 | Q18120 | Q18120 caenorhabdi |
| 44 | 255 | 9.2 | 452 | 5 | Q93531 | Q93531 caenorhabdi |
| 45 | 253.5 | 9.2 | 270 | 11 | Q9JL57 | Q9jl57 cavia porce |

ALIGNMENTS

```
RESULT 1
Q8BUW1
ID   Q8BUW1        PRELIMINARY;      PRT;   535 AA.
AC   Q8BUW1;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Potassium channel subfamily K member 10.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Cerebellum;
RX   MEDLINE=22354683; PubMed=12466851;
RA   The FANTOM Consortium;
RA   the RIKEN Genome Exploration Research Group Phase I & II Team;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573 (2002).
DR   EMBL; AK082153; BAC38424.1; -.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005267; F:potassium channel activity; IEA.
DR   GO; GO:0006811; P:potassium ion transport; IEA.
DR   InterPro; IPR003280; K-channel_2pore.
DR   InterPro; IPR001622; K-channel_pore.
DR   InterPro; IPR003976; Trek_channel.
DR   PRINTS; PR01333; 2POREKCHANEL.
DR   PRINTS; PR01499; TREKCHANNEL.
SQ   SEQUENCE 535 AA; 59401 MW; 3E98B89F875C26BD CRC64;

Query Match             93.4%;    Score 2578.5;  DB 11;  Length 535;
Best Local Similarity   93.9%;    Pred. No. 1.2e-180;
Matches 508;  Conservative  11;  Mismatches  13;  Indels  9;  Gaps  3;

Qy    1 MFFLYTDFFL--SLVAVPAAA-PVCQPKSATNGQPPAPAPTPTPRLSISSRATVVARMEG 57
          :|| .| :|.:   ||||||||  |||||||||||      ||||||||||||||||||
Db    1 MYFSYIGYFFLPPLVAVPAAAPPVCQPKSATNGH-----HPVPRLSISSRATVVARMEG 54
```

```
Matches   433;  Conservative   6;  Mismatches  11;  Indels   9;  Gaps   3;

Qy     1 MFFLYTDFFL--SLVAVPAAA-PVCQPKSATNGQPPAPAPTPTPRLSISSRATVVARMEG  57
         |||||||||||  :|||||||  | :|: : |  :                 |||||||||||
Db     1 MYFSYIGYFFLPPLVAPAAAPPVCQPKSATNGH-----HPVPRLSISSRATVVARMEG  54

Qy    58 TSQGGLQTVMKWKTVVAIFVVVVYLVTGGLVFRALEQPFESSQKNTIALEKAEFLRDHV  117
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    58 TSQGGLQTVMKWKTVVAIFVVVVYLVTGGLVFRALEQPFESSQKNTIALEKAEFLRDHV  117

Qy   118 CVSPQELETLIQHALDADNAGVSPIGNSSNNSSHWDLGSAFFFAGTVITTIGYGNIAPST  177
         |||||||||||||||||||||||::|||| :||||||||||||||||||||||||||||
Db   115 CVSPQELETLIQHALDADNAGVSPVGNSSNSSSHWDLGSAFFFAGTVITTIGYGNIAPST  174

Qy   178 EGGKIFCILYAIFGIPLFGFLLAGIGDQLGTIFGKSIARVEKVFRKKQVSQTKIRVISTI  237
         |||||||||||||||||||||||||||||||||||||||||||||:||||||||||||||
Db   175 EGGKIFCILYAIFGIPLFGFLLAGIGDQLGTIFGKSIARVEKVFRKKQVSQTKIRVISTI  234

Qy   238 LFILAGCIVFVTIPAVIFKYIEGWTALESIYFVVVTLTTVGFGDFVAGGNAGINYREWYK  297
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   235 LFILAGCIVFVTIPAVIFKYIEGWTALESIYFVVVTLTTVGFGDFVAGGNAGINYREWYK  294

Qy   298 PLVWFWILVGLAYFAAVLSMIGDWLRVLSKKTKEEVGEIKAHAAEWKANVTAEFRETRRR  357
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   295 PLVWFWILVGLAYFAAVLSMIGDWLRVLSKKTKEEVGEIKAHAAEWKANVTAEFRETRRR  354

Qy   358 LSVEIHDKLQRAATIRSMERRRLGLDQRAHSLDMLSPEKRSVFAALDTGRFKASSQESIN  417
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   355 LSVEIHDKLQRAATIRSMERRRLGLDQRAHSLDMLSPEKRSVFAALDTGRFKASSQESIN  414

Qy   418 NRPNNLRLKGPEQLNKHGQGASEDNIINKFGSTSRLIKR  456
         |||||||||||||||||:::|||||||||||||||::||
Db   415 NRPNNLRLKGPEQLTKHGQGAFEDNIINKFGSTSKLTKR  453

Qy   538 N  538
         |
Db   535 N  535
```

RESULT 2
```
Q8BZB0
ID   Q8BZB0           PRELIMINARY;        PRT;       453 AA.
AC   Q8BZB0;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Potassium channel subfamily K member 10 (Fragment).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Cerebellum;
RX   MEDLINE=22354683; PubMed=12466851;
RA   the FANTOM Consortium,
RA   the RIKEN Genome Exploration Research Group Phase I & II Team;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573 (2002).
DR   EMBL; AK036066; BAC29295.1; -.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005267; F:potassium channel activity; IEA.
DR   GO; GO:0006813; P:potassium ion transport; IEA.
DR   InterPro; IPR003280; K+channel_2pore.
DR   InterPro; IPR001622; K+channel_pore.
DR   InterPro; IPR003976; Trek_channel.
DR   PRINTS; PR01333; 2POREKCHANNEL.
DR   PRINTS; PR01499; TREKCHANNEL.
FT   NON_TER       453    453
SQ   SEQUENCE   453 AA;  49958 MW;  F8CSC3FF41E823E0 CRC64;
```

Query Match             79.0%;  Score 2180.5;  DB 11;  Length 453;
Best Local Similarity   94.3%;  Pred. No. 1.5e-151;

```
Qy    58 TSQGGLQTVMKWKTVVAIFVVVVYLVTGGLVFRALEQPFESSQKNTIALEKAEFLRDHV  117
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    55 ASQGGLQTVMKWKTVVAIFVVVVYLVTGGLVFRALEQPFESSQKNTIALEKAEFLRDHI  114

Qy   118 CVSPQELETLIQHALDADNAGVSPIGNSSNNSSHWDLGSAFFFAGTVITTIGYGNIAPST  177
         ||||||||||||||||||||||||:|||| :|||||||||||||||||||||||||||||
Db   115 CVSPQELETLIQHALDADNAGVSPVGNSSNSSSHWDLGSAFFFAGTVITTIGYGNIAPST  174

Qy   178 EGGKIFCILYAIFGIPLFGFLLAGIGDQLGTIFGKSIARVEKVFRKKQVSQTKIRVISTI  237
         |||||||||||||||||||||||||||||||||||||||||||||:||||||||||||||
Db   175 EGGKIFCILYAIFGIPLFGFLLAGIGDQLGTIFGKSIARVEKVFRKKQVSQTKIRVISTI  234

Qy   238 LFILAGCIVFVTIPAVIFKYIEGWTALESIYFVVVTLTTVGFGDFVAGGNAGINYREWYK  297
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   235 LFILAGCIVFVTIPAVIFKYIEGWTALESIYFVVVTLTTVGFGDFVAGGNAGINYREWYK  294

Qy   298 PLVWFWILVGLAYFAAVLSMIGDWLRVLSKKTKEEVGEIKAHAAEWKANVTAEFRETRRR  357
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   295 PLVWFWILVGLAYFAAVLSMIGDWLRVLSKKTKEEVGEIKAHAAEWKANVTAEFRETRRR  354

Qy   358 LSVEIHDKLQRAATIRSMERRRLGLDQRAHSLDMLSPEKRSVFAALDTGRFKASSQESIN  417
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   355 LSVEIHDKLQRAATIRSMERRRLGLDQRAHSLDMLSPEKRSVFAALDTGRFKASSQESIN  414

Qy   418 NRPNNLRLKGPEQLNKHGQGASEDNIINKFGSTSRLTKRNKDLKKTLPEDVQKIYKTFR  477
         |||||||||||||:||||||||:|||||||||||||:||||||||:|||||||||||||
Db   415 NRPNNLRLKGPEQLTKHGQGASEDNIINKFGSTSKLTKRNKDLKKTLPEDVQKIYKTFR  474

Qy   478 NYSLDEKKEEETEKMCNSDNSSTAMLTDCIQQHAELENGNLPTDTKDREPENNSLLEDR  537
         ||||||||||||||||||||||||||||:|||| |||||| |||||||:|||||||||||
Db   475 NYSLDEKKEDETEKMCNSDNSSTAMLTECIQQQAEMENGMVPTDTKDQGLENNSLLEDR  534

Qy   538 N  538
         |
Db   535 N  535
```

RESULT 3
```
Q920B6
ID   Q920B6           PRELIMINARY;        PRT;       426 AA.
AC   Q920B6;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   2P domain potassium channel KCNK2 (Tandem pore domain potassium
DE   channel TREK-1).
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=21219399; PubMed=11319556;
RA   Bockenhauer D., Zilberberg N., Goldstein S.A.;
RT   "KCNK2: reversible conversion of a hippocampal potassium leak into a
RT   voltage-dependent channel.";
RL   Nat. Neurosci. 4:486-491(2001).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Wistar;
RX   MEDLINE=21896087; PubMed=11897838;
RA   Gu W., Schlichthorl G., Hirsch J.R., Engels H., Karschin C.,
RA   Karschin A., Derst C., Steinlein O.K., Daut J.;
RT   "Expression pattern and functional characteristics of two novel splice
RT   variants of the two-pore-domain potassium channel TREK-2.";
RL   J. Physiol. 539:657-668(2002).
DR   EMBL; AF325671; AAL01159.1; -.
DR   EMBL; AF385402; AAL95708.1; -.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0005216; F:ion channel activity; IEA.
DR   GO; GO:0005267; F:potassium channel activity; IEA.
DR   GO; GO:0006811; P:potassium ion transport; IEA.
DR   InterPro; IPR003280; K+channel_2pore.
DR   InterPro; IPR001622; K+channel_pore.
```

```
DR    InterPro; IPR003976; Trek_channel.
DR    PRINTS; PR01333; 2POREKCHANEL.
DR    PRINTS; PR01499; TREKCHANNEL.
KW    Ionic channel; Transmembrane.
SQ    SEQUENCE   426 AA;  46912 MW;  CACDA05BBE95FDBC CRC64;

Query Match             45.2%;  Score 1247.5;  DB 11;  Length 426;
Best Local Similarity   63.8%;  Pred. No. 3.7e-83;
Matches  245;  Conservative  56;  Mismatches  66;  Indels  17;  Gaps   5;

Qy     17  AAAPVCQPKSATNGQPPAPAPTPTPRLSISSRATVVA-RMEGTSQGGLQTVMKKTVVAI  75
               :|||||:| :|| :::| |:|  |  |  | ||  |  | |||||| ||  ||||||
Db     17  AAPDLLDPKSA-------AQNSKPRLSFSAKPTVLASRVESDS--AINVMKWKTVSTI  65

Qy     76  FVVVVYLVTGGLVPRALEQPFESSQKNTIALEKAEFLRDHVCVSPQELETLIQHALDAD 135
               |:|||:|: ||||::|||::| ::|:|||:|::|  | ::| ||:: |::|||:||:
Db     66  FLVVVLYLIIGATVFKALEQPQEISQRTTIVIQKQNFIAQHACVNSTELDELIQQIVTAI 125

Qy    136  NAGVSPIGNSSNNSSHWDLGSAFFFAGTVITTIGYGNIAPSTEGGKIFCILYAIFGIPLF 195
               ||| |||||:|:||||||||::|||||||||||||||| || ||||||||:||||||||
Db    126  NAGIIPLGNSNQVSHWDLGSSFFFAGTVITTIGFGNISPRTEGGKIFCIIYALLGIPLF 185

Qy    196  GFLLAGIGDQLGTIFGKSIARVEKVFRKKQVSQTKIRVISTILFILAGCIVFVTIPAVIF 255
               |||||||||||||||||: |||||:|||||||| ||||:||||||: ::||: |||||||
Db    186  GFLLAGVGDQLGTIFGKGIAKVEDTFIKMWNVSQTKIRIISTIIFILFGCVLFVALPAVIF 245

Qy    256  KYIEGWTALESIYFVVVITTVGFGDFVAGGNAGINYREWYKPLVWFWILVGLAYFAAVL 315
               ||||||:|||:|||||:||::|||||||||||||||::| |:|::::|||||:||||||
Db    246  KHIEGWSALDAIYFVVITTIGFGDYVAGG-SDIEYLDFYKPVVWFWILVGLAYFAAVL 304

Qy    316  SMIGDWLRVLSKKTKEEVGEIKAHAAEWKANVTAEFRETRRRLSVEIHDKLQRAATIRSM 375
               |||||||||:|||||||||||||| |:|||||||||||||||||||:|::|:|||||:
Db    305  SMIGDWLRVISKKTKEEVGEFRAHAAEWTANVTAEFKETRRRLSVEIIYDKFQRATSV--- 361

Qy    376  ERRRLGLDQRAHSLDMLSPEKRSV 399
               :|:  |:|||:::|:|| :|:
Db    362  -KRKLSAELAGNHNQELTPCRRTL 384
```

```
RESULT 4
Q8HY88
ID    Q8HY88;          PRELIMINARY;     PRT;     411 AA.
AC    Q8HY88;
DT    01-MAR-2003 (TrEMBLrel. 23, Created)
DT    01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT    01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE    Potassium channel subfamily K member 2.
GN    KCNK2.
OS    Bos taurus (Bovine).
OC    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC    Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC    Bovidae; Bovinae; Bos.
OX    NCBI_TaxID=9913;
RN    [1]
RP    SEQUENCE FROM N.A.
RC    TISSUE=Adrenal cortex;
RX    PubMed=12368289;
RA    Enyeart J.J., Xu L., Danthi S., Enyeart J.A.;
RT    "An ACTH- and ATP-regulated Background K+ Channel in Adrenocortical
RT    Cells Is TREK-1.";
RL    J. Biol. Chem. 277:49186-49199(2002).
EMBL; AY148474; AAN37591.1; -.
GO; GO:0015020; C:membrane; IEA.
GO; GO:0005267; F:potassium channel activity; IEA.
GO; GO:0006813; P:potassium ion transport; IEA.
InterPro; IPR003280; K+channel_2pore.
InterPro; IPR003976; Trek channel.
PRINTS; PR01333; 2POREKCHANEL.
PRINTS; PR01499; TREKCHANNEL.
SQ    SEQUENCE   411 AA;  45438 MW;  A18SEAC20A68CCDC CRC64;

Query Match             45.1%;  Score 1244.5;  DB 6;  Length 411;
```

```
Best Local Similarity   63.5%;  Pred. No. 5.8e-83;
Matches  244;  Conservative  57;  Mismatches  66;  Indels  17;  Gaps   5;

Qy     17  AAAPVCQPKSATNGQPPAPAPTPTPRLSISSRATVVA-RMEGTSQGGLQTVMKKTVVAI  75
               :|||||:| :|| :::| |:|  |  |  | ||  |  | |||||| ||  ||||||
Db      2  AAPDLLDPKSA-------AQNSKPRLSFSFSTKPTVLASRVESDT--TINVMKWKTVSTI  50

Qy     76  FVVVVYLVTGGLVPRALEQPFESSQKNTIALEKAEFLRDHVCVSPQELETLIQHALDAD 135
               |:|||:|: ||||::|||::| ::|:|||:|::|  | ::| ||:: |::|||:||:
Db     51  FLVVVLYLIIGATVFKALEQPHEISQRTTIVIQKQTFISQHACVNSTELDELIQQIVAAI 110

Qy    136  NAGVSPIGNSSNNSSHWDLGSAFFFAGTVITTIGYGNIAPSTEGGKIFCILYAIFGIPLF 195
               ||| |||||:|:||||||||::|||||||||||||||| || ||||||||:||||||||
Db    111  NAGIIPLGNSNQISHWDLGSSFFFAGTVITTIGFGNISPRTEGGKIFCIIYALLGIPLF 170

Qy    196  GFLLAGIGDQLGTIFGKSIARVEKVFRKKQVSQTKIRVISTILFILAGCIVFVTIPAVIF 255
               |||||||||||||||||: |||||:|||||||| ||||:||||||: ::||: |||||||
Db    171  GFLLAGVGDQLGTIFGKGIAKVEDTFIKMWNVSQTKIRIISTIIFILFGCVLFVALPAIIF 230

Qy    256  KYIEGWTALESIYFVVVITTVGFGDFVAGGNAGINYREWYKPLVWFWILVGLAYFAAVL 315
               ||||||:|||:|||||:||::|||||||||||||||::| |:|::::|||||:||||||
Db    231  KHIEGWSALDAIYFVVITTIGFGDYVAGG-SDIEYLDFYKPVVWFWILVGLAYFAAVL 289

Qy    316  SMIGDWLRVLSKKTKEEVGEIKAHAAEWKANVTAEFRETRRRLSVEIHDKLQRAATIRSM 375
               |||||||||:|||||||||||||| |:|||||||||||||||||||:|::|:|||||:
Db    290  SMIGDWLRVISKKTKEEVGEFRAHAAEWTANVTAEFKETRRRLSVEIIYDKFQRATSI--- 346

Qy    376  ERRRLGLDQRAHSLDMLSPEKRSV 399
               :|:  |:|||:::|:|| :|:
Db    347  -KRKLSAELAGNHNQELTPCRRTL 369
```

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RESULT 5
Q9NRT2
ID    Q9NRT2;          PRELIMINARY;     PRT;     411 AA.
AC    Q9NRT2;
DT    01-OCT-2000 (TrEMBLrel. 15, Created)
DT    01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT    01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE    Two-pore domain potassium channel TREK-1.
GN    TREK-1.
OS    Homo sapiens (Human).
OC    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX    NCBI_TaxID=9606;
RN    [1]
RP    SEQUENCE FROM N.A.
RC    TISSUE=Brain;
RX    MEDLINE=20244931; PubMed=10784345;
RA    Meadows H.J., Benham C.D., Cairns W., Gloger I.S., Jennings C.,
RA    Medhurst A.D., Murdock P., Chapman C.G.;
RT    "Cloning, localisation and functional expression of the human
RT    orthologue of the TREK-1 potassium channel.";
RL    Pflugers Arch. 439:714-722(2000).
EMBL; AF171068; AAF89743.1; -.
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0005216; F:ion channel activity; IEA.
GO; GO:0005267; F:potassium channel activity; IEA.
GO; GO:0006813; P:potassium ion transport; IEA.
InterPro; IPR003280; K+channel_2pore.
InterPro; IPR001622; K+channel_pore.
InterPro; IPR003976; Trek channel.
PRINTS; PR01333; 2POREKCHANEL.
PRINTS; PR01499; TREKCHANNEL.
KW    Ionic channel; Transmembrane.
SQ    SEQUENCE   411 AA;  45494 MW;  FDE40CAB21B42A1C CRC64;

Query Match             45.0%;  Score 1242.5;  DB 4;  Length 411;
Best Local Similarity   63.5%;  Pred. No. 8.2e-83;
Matches  244;  Conservative  57;  Mismatches  66;  Indels  17;  Gaps   5;

Qy     17  AAAPVCQPKSATNGQPPAPTPTPRLSISSRATVVA-RMEGTSQGGLQTVMKKTVVAI  75
               :|||||:| :|| :::| |:|  ||  |  | ||  |  | |||||| ||  ||||||
```

Query Match       35.6%;   Score 983.5;   DB 11;   Length 241;
Best Local Similarity   93.4%;   Pred. No. 3.9e-64;
Matches  197;   Conservative   3;   Mismatches   4;   Indels   7;   Gaps   2;

Qy    13  VAVPAAA-PVCQPKSATNGQPPAPAPTPTPRLSISSRATVVARMEGTSQGGLQTVMKWKT  71
              |||:||| :||:|||||| :            ||||||||||:|||||:|: |||||||||
Db    18  VAVPAAAPPVCQPKSATNGH-----HPVPRLSISSRATVVARMEGASQGGLQTVMKWKT  71

Qy    72  VVAIFVVVVYLVTGLVFRALEQPFESSQKNTIALEKAEFLRDHVCVSPQELETLIQHA  131
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    72  VVAIFVVVVYLVTGLVFRALEQPFESSQKNTIALEKAEFLRDHICVSPQELETLIQHA  131

Qy   132  LDADNAGVSPIGNSNNSSHWDLGSAFFFAGTVTTIGYGNIAPSTEGGKIFCILYAIFG  191
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   132  LDADNAGVSPVGNSSNNSSHWDLGSAFFFAGTVTTIGYGNIAPSTEGGKIFCILYAIFG  191

Qy   192  IPLFGFLLAGIGDQLGTIFGKSIARVEKVFR  222
              ||||||||||||||||||||||||||||||
Db   192  IPLFGFLLAGIGDQLGTIFGKSIARVEKVPR  222

RESULT 7
Q8BWJ6
ID   Q8BWJ6           PRELIMINARY;        PRT;    193 AA.
AC   Q8BWJ6;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Potassium channel subfamily K member 10 (Fragment).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Heart;
RX   MEDLINE=22354683; PubMed=12466851;
RA   The FANTOM Consortium,
RA   the RIKEN Genome Exploration Research Group Phase I & II Team;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
DR   EMBL; AK052327; BAC34939.1; -.
FT   NON_TER       1      1
SQ   SEQUENCE   193 AA;   22174 MW;   8CCBADA59EF60641 CRC64;

Query Match       33.7%;   Score 930;   DB 11;   Length 193;
Best Local Similarity   93.8%;   Pred. No. 2.4e-60;
Matches  181;   Conservative   7;   Mismatches   5;   Indels   0;   Gaps   0;

Qy   346  NVTAEFRETRRRLSVEIHDKLQRAATIRSMERRRLGLDQRAHSLDMLSPEKRSVFAALDT  405
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1  NVTAEFREARRRLSVEIHDKLQRAATIRSMERRRLGLDQRAHSLDMLSPEKRSVFAALDT  60

Qy   406  GRFKASSQESINNRPNNLRLKGPEQLNKHGQGASEDNIINKFGSTSRLTKRKNKDLKKTL  465
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61  GRFKASSQESINNRPNNLRLKGPEQLTKHGQGASEDNIINKFGSTSKLTKRKNKDLKKTL  120

Qy   466  PEDVQKIYKTFRNYSLDEKKEETERMCNSDNSSTAMLTDCIQQHAELENGMIPTDTKD  525
              |||||||:||||||||||||||:|||||||||||||||||||||:||||||||||||
Db   121  PEDVQKIYRTFRNYSLDEKKEDETERMCNSDNSSTAMLTECIQQQAEMENGMVPTDTKD  180

Qy   526  REPENNSLLEDRN  538
              :|||||||||||
Db   181  QGLENNSLLEDRN  193

RESULT 8
Q92414
ID   Q92414           PRELIMINARY;        PRT;    397 AA.
AC   Q92414;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)

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Db     2  AAPDLLDPKSA-------AQNSKPRLSFSTKPTVLASRVESDT---TINVMKWKTVSTI   50

Qy    76  FVVVVYLVTGLVFRALEQPFESSQKNTIALEKAEFLRDHVCVSPQELETLIQHALDAD  135
              |:|:|||: |: |||||||||||||||||||||||||||||||||:||||||||||:
Db    51  FLVVVLYLIIGATVFKALEQPHEISQRTTIVIQKQTFISQHSCVNSTELDELIQQIVAAI  110

Qy   136  NAGVSPIGNSNNSSHWDLGSAFFFAGTVTTIGYGNIAPSTEGGKIFCILYAIFGIPLF  195
              ||| ||||| :|: ||||||:||||| |:|||||||| |: :| |||| ||||| |||
Db   111  NAGIIPLGNTSNQISHWDLGSSFFFAGTVTTIGFGNIAPSPRTEGGKIFCIIYALLGIPLF  170

Qy   196  GFLLAGIGDQLGTIFGKSIARVEKVFRKKQVSQTKIRVISTLFILAGCIVFVTIPAVIF  255
              ||||| ||||||||||||| :|||:|:| :||||||| |||||:||:| |: || |:|
Db   171  GFLLAGVGDQLGTIFGKGIAKVEDTFIKWNVSQTKIRIISTIIFILFGCVLFVALPAIIF  230

Qy   256  KYIEGWTALESIYFVVVTLTTVGFGDFVAGGNAGINYREWYKPLVWFWILVGLAYPAAVL  315
              |:|| |: |:|| |||: |||||| ||||:|:|| |||  :||  :||:||||||||||
Db   231  KHIEGWSALDAIYFVVITLTTIGFGDYVAGG--SDIEYLDFYKPVVWFWILVGLAYPAAVL  289

Qy   316  SMIGDWLRVLSKKTKEEVGEIKAHAAEBWKANVTAEFRETRRRLSVEIHDKLQRAATIRSM  375
              ||||||||| |||||||||| |: |||:|||||||||:||||||||||||||||||| |
Db   290  SMIGDWLRVISKKTKEEVGEFRAHAAEWTANVTAEFKETRRRLSVEIYDKFQRATSI---  346

Qy   376  ERRRLGLDQRAHSLDMLSPEKRSV  399
              :||  |:|| |:|: |:
Db   347  -KRKLSAELAGNHNQELTPCRRTL  369

RESULT 6
Q9CX88
ID   Q9CX88           PRELIMINARY;        PRT;    241 AA.
AC   Q9CX88;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   3010005K24Rik protein.
GN   3010005K24RIK.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Embryo;
RX   MEDLINE=21085660; PubMed=11217851;
RA   Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA   Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA   Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA   Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA   Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA   Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA   Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA   Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA   Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA   Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA   Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA   Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA   Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA   Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA   Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA   Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA   Hayashizaki Y.;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
DR   EMBL; AK019376; BAB31686.1; -.
DR   MGD; MGI:1924704; 3010005K24Rik.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005267; F:potassium channel activity; IEA.
DR   GO; GO:0006813; P:potassium ion transport; IEA.
DR   InterPro; IPR001622; K=channel_pore.
DR   InterPro; IPR003976; Trek_channel.
DR   PRINTS; PR01499; TREKCHANNEL.
SQ   SEQUENCE   241 AA;   25799 MW;   B4C39F77CD0A39DA CRC64;

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DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Mechanosensitive tandem pore potassium channel.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Sprague-Dawley;
RX   MEDLINE=21268449; PubMed=11374070;
RA   Kim Y., Bang H., Gnatenco C., Kim D.;
RT   "Synergistic interaction and the role of C-terminus in the activation
RT   of TRAAK K+ channels by pressure, free fatty acids and alkali.";
RL   Pflugers Arch. 442:64-72(2001).
DR   EMBL; AF302842; AAK60504.2; -.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005216; F:ion channel activity; IEA.
DR   GO; GO:0005267; F:potassium channel activity; IEA.
DR   GO; GO:0006813; P:potassium ion transport; IEA.
DR   InterPro; IPR001990; Granin.
DR   InterPro; IPR003280; K+channel_2pore.
DR   InterPro; IPR001622; K+channel_pore.
DR   InterPro; IPR008074; TRAAK_channel.
DR   Pfam; PF01271; Granin; 1.
DR   PRINTS; PR01333; 2POREKCHANEL.
DR   PRINTS; PR01691; TRAAKCHANNEL.
KW   Ionic channel.
SQ   SEQUENCE   397 AA;  42987 MW;  3AF04C43FA982D22 CRC64;

Query Match             28.2%;
Best Local Similarity   51.2%;             Score 778;  DB 11;  Length 397;
Matches  150;  Conservative   56;  Mismatches   81;  Pred. No. 9.2e-49;  Indels    6;  Gaps    3;

Qy     67 MKWKTVVAIFVVVVVVLVTGGLVFRALEQPFESSQKNTIALEKAEFLRDHVCVSPQELET 126
             |:|:  :| |::||||  ||— || :  : :|:|| : |
Db      1 MRSTTLLALLALVLLYLVSGALVFFALEQPHEQQVQKDLEDGRDQFLKDHPCVSQKNLEG 60

Qy    127 LIQHALDADNAGVSP---IGNSSNNSSHWDLGSAFFFAGTVITTIGYGNIAPSTEGGKIF 183
              :|| |::||||||||
Db     61 FIKLVAEALGGGANFBTSWTNSSNHSSAWNLGSAFFFSGTIITTIGYGNIALHTDAGRLF 120

Qy    184 CILYAIFGIPLFGFLLAGIGDQLGTIFGKSIARVEKVFRKKQVSQTKIRVISTILFILAG 243
             ||:|| :|||||| ||| || :   |  |: |  : : : |   :|||||||| :|:|
Db    121 CIFYALVGIPLFGMLLAGVGDRLGSSLRRGIGHIEAVFLKWHVPGLVRMLSAVLFLLIG 180

Qy    244 CIVFVTIPAVIFKYIEGWTALESIYFVVVLTTVGFGDFVAGGNAGINYREWYKPLVWFW 303
             |:: || :|: |||:||||||||
Db    181 CLLFVLTPTFVFSYMKSWSKLKAIYFVIVLTTVGFGDYVPGDGYVPGDGTGQN-SPAYQPLVWFW 239

Qy    304 ILVGLAYFAAVLSMIGDWLRVLSKKTKEEVGEIKAHAAEWKANVTAEFRETRR 356
             ||:|||||:|: :|||||:|::|:|:|||
Db    240 ILFGLAYFASVFTTIGNWLRAVSRRTRAEMGGLTAQAASWTGTVTA--RVTQR 290

RESULT 9
Q9JK62
ID   Q9JK62      PRELIMINARY;      PRT;   502 AA.
AC   Q9JK62;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Potassium channel TASK2 (TASK2 potassium channel).
GN   KCNK5.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=129/SvJ; TISSUE=Kidney;
RA   Roux J., Barhanin J.;
RT   "Mouse two P domain potassium channel TASK2.";
```

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RL   Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Kidney;
RA   Cid L.P., Niemeyer M.I., Sepulveda F.V.;
RT   "Functional properties of mouse TASK-2 potassium channel.";
RL   Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Kidney;
RX   MEDLINE=22354683; PubMed=12466851;
RA   The FANTOM Consortium,
RA   the RIKEN Genome Exploration Research Group Phase I & II Team;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573 (2002).
DR   EMBL; AF259395; AAF68668.1; -.
DR   EMBL; AF319542; AAG35065.1; -.
DR   EMBL; AK085330; BAC39423.1; -.
DR   MGD; MGI:1336175; Kcnk5.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005216; F:ion channel activity; IEA.
DR   GO; GO:0005267; F:potassium channel activity; IEA.
DR   GO; GO:0006811; P:potassium ion transport; IEA.
DR   InterPro; IPR003280; K+channel_2pore.
DR   InterPro; IPR001622; K+channel_pore.
DR   InterPro; IPR003092; TASK_channel.
DR   PRINTS; PR01333; 2POREKCHANEL.
DR   PRINTS; PR01095; TASKCHANNEL.
KW   Ionic channel.
SQ   SEQUENCE   502 AA;  55976 MW;  E4C7E7CC71B44D95 CRC64;

Query Match             17.3%;             Score 478.5;  DB 11;  Length 502;
Best Local Similarity   27.0%;             Pred. No. 1.2e-26;
Matches  126;  Conservative   76;  Mismatches  185;  Indels  185;  Gaps   79;

Qy     79 VVVLVTGGLVFRALEQPFESSQKNTIALEKAEFLRDHVCVSPQELETLIQHALDADNAG 138
             :::|  :| |:  ||:|||
Db     12 IIFYLAIGAAIFEVLEEPHWKEAKKNYYTQKLHLLKEFPCLSQEGLDKILQVVSDAADQG 71

Qy    139 VSPIGNSSNNSSHWDLGSAFFFAGTVITTIGYGNIAPSTEGGKIFCILYAIFGIPLFGFL 198
              :  :  ::    :|||||| ||||||||||||||:|||||:  |: :: :|||||
Db     72 VAITGNQTFN--NWNWPNAMIFAATVITTIGYGNVAPKTPAGRLFCVFVGLFGVPL---C 126

Qy    199 LAGIGDQLGTIFGKSIARVEKVFRKKQVSQTKIRVISTILFILAGCIVFVTIPAVIFKYI 258
             |:  ::: :: : :: :| | ||  |:|||::: |:  :||
Db    127 LTWI-SALGKFFGGRAKRLGQFLTRRGVSLRKAQITCTAIFIVWGVLVHLVIPPVFMVT 185

Qy    259 EGWTALESIYFVVVLTTVGFGDFVAGGNAGINYREWYKPLVWFWILVGLAYFAAVLSMI 318
             |     ||:|  :|||:||||||||||||
Db    186 EEWNYIEGLYYSFITISTIGFGDFVAGVNPSANTHALYRYFVELWIYLGLA-------- 236

Qy    319 GDWLRVLSKKTKEEVGEIKAHAAEWKANVTAEFRETRRLSVEIHDKLQRAATIRSMERR 378
              ||:         :::  ::   :::       :: :  : ::
Db    237 --WLSLF--------------VNWKVS-----------MFVEVHKAIK------KRRRRR 263

Qy    379 RLGLDQRAHSLDMLSPEKRSVFAALDTGRFKASSQESINNRPNNL---------RLK 426
              : |:
Db    264 KESFESSPHSRKALQMAGSTASKDVNIFSLSKKEETYNDLIKQIGKKAMKTSGGGERVP 323

Qy    427 GPEQLNKHGQGASEDNIINKFGSTSRLTKRKNKDLKKTLPEDVQKIYKTFRNYSLDEKK 486
             ||   :|:|   :   |:   ::|: :  |:     | || :: :|
Db    324 GP----GHGLGPQGDRLPTIPASLAPLVVYS---KNRVP-SLEEVSQTLKNKGHVSRPL 374

Qy    487 EEETKKMCNSDNSSTAML----TDCIQQHAELENGMIPTDTKDREP 528
             :|  ::      :|::      : :||
Db    375 GEEAGAQAPKDSYQTSEVFINQLDRISEEGG------PWEALDYHP 414

RESULT 10
Q80XE0
ID   Q80XE0      PRELIMINARY;      PRT;   257 AA.
AC   Q80XE0;
```

DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Similar to potassium channel, subfamily K, member 5 (Fragment).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=FVB/N; TISSUE=Colon;
RA   Strausberg R.;
RL   Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC051088; AAH51088.1; -.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005216; F:ion channel activity; IEA.
DR   GO; GO:0005267; F:potassium channel activity; IEA.
DR   GO; GO:0006813; P:potassium ion transport; IEA.
DR   InterPro; IPR003280; K+channel_pore.
DR   InterPro; IPR001622; K+channel_pore.
DR   InterPro; IPR003092; TASK_channel.
DR   PRINTS; PR01333; 2POREKCHANEL.
DR   PRINTS; PR01095; TASKCHANNEL.
KW   Ionic channel.
FT   NON_TER      257    257
SQ   SEQUENCE   257 AA;  29001 MW;  AA00FB0415212GC4 CRC64;

Query Match             16.4%;  Score 454;  DB 11;  Length 257;
Best Local Similarity   37.4%;  Pred. No. 3e-25;
Matches   91;  Conservative   47;  Mismatches   95;  Indels   10;  Gaps   4;

Qy    79  VVVYLVTGGLVFRALEQPFESSQKNTIALEKAEFLRDHVCVSPQELETLIQHALDADNAG 138
              |  ||   :|.|:: |:|::  |: |:: :|| :|:| : ||| |
Db    12  IIFYLAIGAAIFEVLEEPHWKEAKKNYYTQKHLLKEFPCLSQEGLDKILQVVSDAADQG  71

Qy   139  VSPIGNSSNNSSHWDLGSAFFPAGTVITTIGYGNIAPSTEGGKIFCILYAIFGIPLFGFL 198
              |:  || ||  :|: |||||||||||||||||||||||||||||
Db    72  VAITGNQTFN--NWNWPNAMIFAATVITTIGYGNVAPKTPAGRLFCVFYGLFGVPL---C 126

Qy   199  LAGIGDQLGTIFGKSIARVEKVFRKKQVSQTKIRVISTILRFILAGCIVFVTIPAVIFKYI 258
              | ||| :|:|:: ||:|  |||||     ||  : :  ||  :  : :|
Db   127  LTWI-SALGKFPGGGRAKRLGQFLTRRGVSLRKAQITCTAIFIVWGVLVHLVIPPVFMVT 185

Qy   259  EGWTALESIYFVVVTLTTVGFGDFVAGGNAGINYREWYKPLVWFWILVGLAYFAAVLSMI 318
              :|: :||:.|: |  : |  |||   |:| |   | | : ||  :  :|  :|:||
Db   186  EEWNYIEGLYYSFITISTIGFGCDFVAGVNPSANYHALYRYPVELWIYLGLAW---LSLF 241

Qy   319  GDW 321
              :|
Db   242  VNW 244

RESULT 11
Q8N4V5
ID   Q8N4V5             PRELIMINARY;      PRT;   184 AA.
AC   Q8N4V5;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Similar to potassium channel, subfamily K, member 4.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RA   Strausberg R.;
RL   Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC033577; AAH33577.1; -.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005216; F:ion channel activity; IEA.
DR   GO; GO:0005267; F:potassium channel activity; IEA.

DR   GO; GO:0006813; P:potassium ion transport; IEA.
DR   InterPro; IPR001622; K+channel_pore.
DR   InterPro; IPR003976; Trek_channel.
DR   PRINTS; PR01499; TREKCHANNEL.
KW   Ionic channel.
SQ   SEQUENCE   184 AA;  19380 MW;  A9GA6B586D40AFF0 CRC64;

Query Match             16.2%;  Score 447;  DB 4;  Length 184;
Best Local Similarity   44.6%;  Pred. No. 6.1e-25;
Matches   91;  Conservative   29;  Mismatches   54;  Indels   30;  Gaps   2;

Qy    20  PVCQPKSATNGQPPAPAPTPTPRLSISSRATVARMEGTSQGGLQTVMKWKTVVAIFVVV  79
              :   : :  |                              .:::|: :|:| :::|
Db     8  PPARPLQAGSGAGPAPG---------------------------RAMRSTTLALLALV  39

Qy    80  VVYLVTGGLVFRALEQPFESSQKNTIALEKAEFLRDHVCVSPQELETLIQHALDADNAGV 139
              :|:|||||  :|| |:||   | ||  |||:|||:  ||    ||| |
Db    40  LLYLVSGALVFRALEQPHEQQAQRELGEVREKFLRAHPCVSDQELGLLIKEVADALGGGA  99

Qy   140  SPIGNSSNNSSH--WDLGSAFFAGTVITTIGYGNIAPSTEGGKIFCILYAIFGIPLFGF 197
              || |:||||:     | || |||||||||||||||  |: |||||||
Db   100  DPETNSTSNSSHSAWDLGSAFFFSGTIITTIGYGNVALRTDAGRLFCIFYALVGIPLFGI 159

Qy   198  LLAGIGDQLGTIFGKSIARVEKVF 221
              |||| | | | ::|:  || | :
Db   160  LLAGVGDRLGSSLRHGIGHIEAIF 183

RESULT 12
Q8HZT2
ID   Q8HZT2             PRELIMINARY;      PRT;   341 AA.
AC   Q8HZT2;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Potassium channel TASK-4.
GN   KCNK17.
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Derst C., Renigunta V.K., Preisig-Mueller R., Rajan S., Daut J.;
RT   "Cloning and sequencing of bovine potassium channel TASK-4.";
RL   Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF479760; AAN32894.1; -.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005267; F:potassium channel activity; IEA.
DR   GO; GO:0006813; P:potassium ion transport; IEA.
DR   InterPro; IPR003280; K+channel_2pore.
DR   InterPro; IPR001622; K+channel_pore.
DR   InterPro; IPR003092; TASK_channel.
DR   PRINTS; PR01333; 2POREKCHANEL.
DR   PRINTS; PR01095; TASKCHANNEL.
SQ   SEQUENCE   341 AA;  37695 MW;  0A21FEEA71B39401 CRC64;

Query Match             15.4%;  Score 424.5;  DB 6;  Length 341;
Best Local Similarity   34.2%;  Pred. No. 6.4e-23;
Matches   96;  Conservative   58;  Mismatches   120;  Indels   7;  Gaps   4;

Qy    39  PTPRLSISSRATVARMEGTSQGGLQ-TVMKWKTVVAIFVVVVYLVTGGLVFRALEQPF  97
              |:|||||||| |||||||||||| .:  : :: :    : |:|| ||  ::||: :|:
Db     3  PDSRLS-ASPAKSGWRAWNASERGVQGCAVPVPSTLLLLITVILTYLVLGTCVFWALSSPA  61

Qy    98  ESSQKNTIALEKAEFLRDHVCVSPQELETLIQHALDADNAGVSPIGNSSNNSSHWDLGSA 157
              :||||||||||||||||||||||||||||||||||||||||  ||| ||||||:|||||
Db    62  AHDSKRFQRDKWALLRNFTCLDGQALDSLIRGIIEAYKNGDIVLGNNT-SMGRWEFVGS 120

Qy   158  FFFAGTVITTIGYGNIAPSTEGGKIFCILYAIFGIPLFGFLLAGIGDQLGTIFGKSIARV 217
              || ||||||||||||:   : |   : : :::: |: |  : :|:  |:  :: :
Db   121  FFFSVSTITTIGYGNLSPRTVAARLFCIFFALVGIPLNLVVL----NRLGHCMQQGVHRC 176

```
Qy    218  EKVFRKKQVSQTKIRVISTILFILAGCIVFVTIPAVIFKYIEGWTALESIYFVVVTLTTV  277
                :  |||:::|: ::|:| ::|||::|: ::|| :||.|| |||:||
Db    177  ARRLGGAWKDPAKARWLAGSSALLSGLLLFLILPPLLFNHMEGWTYVEGFYFSFVTLSTV  236

Qy    278  GFGDFVAGNAGINYREWYKPLVWFWILVGLAYFAAVLSMI  318
                ||||||||   |||||: || |||:||  :|:| :||| |
Db    237  GFGDYVIGMNPSRNYPLWYQNTVSLWILFGMAWLALIIKLI  277


RESULT 13
Q801T4
ID    Q801T4        PRELIMINARY;           PRT;      307 AA.
AC    Q801T4;
DT    01-JUN-2003 (TrEMBLrel. 24, Created)
DT    01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT    01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE    Similar to potassium channel, subfamily K, member 6 (TWIK-2).
OS    Xenopus laevis (African clawed frog).
OC    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC    Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC    Xenopodinae; Xenopus.
OX    NCBI_TaxID=8355;
RN    [1]
RP    SEQUENCE FROM N.A.
RC    TISSUE=Embryo;
RA    Klein S., Strausberg R.;
RL    Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
DR    EMBL; BC047247; AAH47247.1; -.
DR    GO; GO:0016021; C:integral to membrane; IEA.
DR    GO; GO:0005216; F:ion channel activity; IEA.
DR    GO; GO:0005267; F:potassium channel activity; IEA.
DR    GO; GO:0006811; P:ion transport; IEA.
DR    GO; GO:0006813; P:potassium ion transport; IEA.
DR    InterPro; IPR005821; Ion_trans.
DR    InterPro; IPR003280; K+channel_2pore.
DR    InterPro; IPR001622; K+channel_pore.
DR    InterPro; IPR001779; TWIK1_channel.
DR    InterPro; IPR005586; TWIK_channel.
DR    Pfam; PF00520; ion_trans; 1.
DR    PRINTS; PR01333; 2POREKCHANEL.
DR    PRINTS; PR01096; TWIK1CHANNEL.
DR    PRINTS; PR01586; TWIKCHANNEL.
KW    Ionic channel.
SQ    SEQUENCE   307 AA;  35190 MW;  E7C4B8B553B94BE9 CRC64;

Query Match             14.6%;
Best Local Similarity   35.2%;
Matches    86;  Conservative    50;  Mismatches   50;  Indels   10;  Gaps    4;

Qy     69  WKTVAIFVVVVVVLVTGGLVFRALEQPFESSQKNTIALEKAEPLRDHVCVSPQELETLI  128
                |||  ||:||:| ||||||||: :|::|| |:|||: | | :||  |:||  ||
Db      4  WLLTLLVCVVVIYLLLGALVISVIESPYEASLRDELRQLKNVFLNESPCVNVSSLEAFL  63

Qy    129  QHALDADNAGVSPIGNSSNNSSHWDLGSAFFFAGTVITTIGYGNIAPSTEGGKIFCILYA  188
                :|||  || | :|||:  ||| :| :||:||||||| |||||:|::|| ||:|:|:||
Db     64  EKIINANKYGVSVLHNASNDSK-WDIASSLFFASTLVTTVGYGYTTPLTDSGKAFCIFYG  122

Qy    189  IFGIPLFGFLLAGIGDQLGTIFGKSIAR--VEKVPRKKQVSQTKIRVISTILFILAGCI  245
                |:|| || || ||||||||||||: :||    :|:|::||: :||||||||| || :
Db    123  LIGVPFTMLVLSSFVQRLMVMFTHKPIRYLQVHRGFDRKMVTQ-----LHFIFLLLVFV  177

Qy    246  VFVTIPAVIFKYIE-GWTALESIYFVVVTLTTVGFGDFVAGGNAGINYREWYKPLVWFWI  304
                ::: ||:||: | ||||||||:| |::|| ||::|| :|| ||:|| |||||| |: |
Db    178  FFLIIPSAIFNTIETSWSFLDAFYFCFISLCTIGLGDYVPGEQNDQWLRKLYKVSVAFYL  237

Qy    305  LVGL  308
           |||
Db    238  FVGL  241


RESULT 14
Q9Z2T2
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```
ID    Q9Z2T2        PRELIMINARY;           PRT;      336 AA.
AC    Q9Z2T2;
DT    01-MAY-1999 (TrEMBLrel. 10, Created)
DT    01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT    01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE    Putative potassium channel TWIK.
OS    Rattus norvegicus (Rat).
OC    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC    Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX    NCBI_TaxID=10116;
RN    [1]
RP    SEQUENCE FROM N.A.
RA    Gan L., Joiner W.J., Quinn A.M., Wang L.-Y., Hughes T.,
RA    Kaczmarek L.K.;
RT    "Cloning and localization of rTWIK, a putative potassium channel with
RT    two P domains.";
RL    Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
DR    EMBL; AF022819; AAD09336.1; -.
DR    GO; GO:0016021; C:integral to membrane; IEA.
DR    GO; GO:0005216; F:ion channel activity; IEA.
DR    GO; GO:0005267; F:potassium channel activity; IEA.
DR    GO; GO:0006813; P:potassium ion transport; IEA.
DR    InterPro; IPR003280; K+channel_2pore.
DR    InterPro; IPR001622; K+channel_pore.
DR    InterPro; IPR001779; TWIK1_channel.
DR    InterPro; IPR005408; TWIK_channel.
DR    PRINTS; PR01333; 2POREKCHANEL.
DR    PRINTS; PR01096; TWIK1CHANNEL.
DR    PRINTS; PR01586; TWIKCHANNEL.
KW    Ionic channel; Transmembrane.
SQ    SEQUENCE   336 AA;  38228 MW;  5E78031947D75DE6 CRC64;

Query Match             14.5%;
Best Local Similarity   30.5%;   Pred. No. 3.9e-21;
Matches   100;  Conservative   60;  Mismatches  108;  Indels   60;  Gaps   11;

Qy     76  FVVV--VVYLVTGGLVFRALEQPFESSQKNTIALEKAEPLRDHVCVSPQELETLIQHALD  133
                ||.:  |||: ::|||| :|::|:| :|||| |:|||    :|:|| :| |||:||||
Db     25  FLVLGYLLYLVFGAVVFSSVELFYEDLLRQELRKLKRRFLEEHECLSEPQLEQFLGRVLE  84

Qy    134  ADNAGVSPIGNSSNNSSHWDLGSAFFFAGTVITTIGYGNIAPSTEGGKIFCILYAIFGIP  193
                |  :||| ::|::||| :|  |||:||||||  |||||:|:| |||| ||||:||||
Db     85  ASNYGVSVLSNASGN-WNWDFTSALFFASTLVSTTGYGHTVPLSDGGKAFCIIYSVIGIP  143

Qy    194  LFGFLLAGIGDQLGTIFGKSIARVEKVFRKKQV--------SQTKIRVISTIL--FILA  242
                ||||| |||||||||||||: |:| :| ::| :         :|||:||| |  :|:|
Db    144  FTLLFLTAV-------------VQRVTVHVTRRPVLYFHIRWGFSKQVVAIVHAVLLGFVTV  192

Qy    243  GCIVFVTIPAVIFKYIE-GWTALESIYFVVVTLTTVGFGDFVAGGNAGINYREWYKPLVW  301
                ||:|| ||:|||::|  ||||||:|  :||:||| ||::|| :||  ||:|| |:|| |
Db    193  SCFFF--IPAAVFSVLEDDWNFLESFYFCFISLSTIGLGDYVPGEGYNQKFRELYKIGIT  250

Qy    302  FWILVGLAYFAAVLSMIGDWLRVLSK----KTKEEVGEIKAHAAEWKANVTAEFRETRR  356
                ||:||||  || |:|||| |:|:|     |||:||| || |:  |:|| |  |::||
Db    251  CYLLLGLIAMLVVLETFCB-LHELKFKRKMFYVVKDKDEDQVHIME-----------  295

Qy    357  RLSVEIHDKL------QRAATIRSMERR  378
                 |:| :| |       :|   |:|| |
Db    296  ------HDQLSFSSITEQRAAGLKEEQKQ  317


RESULT 15
Q8R454
ID    Q8R454        PRELIMINARY;           PRT;      336 AA.
AC    Q8R454;
DT    01-JUN-2002 (TrEMBLrel. 21, Created)
DT    01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT    01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE    Potassium channel TWIK-1.
GN    KCNK1.
OS    Cavia porcellus (Guinea pig).
OC    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC    Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
```

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OX   NCBI_TaxID=10141;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Derst C., Rajan S., Preisig-Mueller R.;
RT   "Cloning and sequencing of guinea pig TWIK channels.";
RL   Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
     EMBL; AY075096; AAL82795.1; -.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0005216; F:ion channel activity; IEA.
DR   GO; GO:0005267; F:potassium channel activity; IEA.
DR   GO; GO:0006813; P:potassium ion transport; IEA.
DR   InterPro; IPR003280; K+channel_2pore.
DR   InterPro; IPR001622; K+channel_pore.
DR   InterPro; IPR001779; TWIK1_channel.
DR   InterPro; IPR005408; TWIK_channel.
DR   PRINTS; PR01333; 2POREKCHANEL.
DR   PRINTS; PR01096; TWIK1CHANNEL.
DR   PRINTS; PR01586; TWIKCHANNEL.
KW   Ionic channel; Transmembrane.
SQ   SEQUENCE   336 AA;  38102 MW;  299B69159D7F5B2A CRC64;
```

```
Query Match          14.4%;  Score 398;  DB 11;  Length 336;
Best Local Similarity   29.8%;  Pred. No. 5.5e-21;
Matches   96;  Conservative   60;  Mismatches  108;  Indels   58;  Gaps   10;

Qy    80 VVYLVTGLVFRALEQPPESSQKNTIALEKAEFLRDHVCVSPQELETLIQHALDADNAGV 139
            ::||||||:  ||  :||     :  :|::|  |  :|  :|   ::|:| |
Db    31 LLYLVFGAVVFSSVELPYEDLLRQELRKLKRFLEEHECLSEPQLEQFLGRVLEASNYGV  90

Qy   140 SPIGNSNNSSHWDLGSAFFFAGTVITTIGYGNIAPSTEGGKIFCILYAIFGIPLFGFLL 199
            |  :|: ||   ||||| ||| |||||:||| || :|  || |||::::|:|| ||
Db    91 SVLSNASGN-WNWDFTSALFFASTVLSTTGYGHTVPLSDGGKAFCIIYSVIGIPFTLLFL 149

Qy   200 AGIGDQLGTIFGKSIARVEKVFRKKQV--------SQTKIRVISTIL--FILAGCIVFV 248
             ::   |:        :   :   :: :      :|:  |: :   ::|
Db   150 TAV--------VQRITVHVTRRPVLYFHIRWGFSKQMVGIVHAVVLGFVTVSCFFF-  197

Qy   249 TIPAVIFKYIE-GWTALESIYFVVVLTTVGFGDFVAGGNAGINYREWYKPLVWFWILVG 307
           :|||||  |  ||||  |::||:::||:|  ||  |  |:|:  ||  :||:|:  :|
Db   198 -IPAAVFSVLEDDWNFLESFYFCFISLSTIGLGDYVPGEGYNQKFRELYKIGITCYLLLG 256

Qy   308 LAYFAAVLSMIGDWLRVLSK----KTKEEVGEIKAHAAEWKANVTAEFRETRRLSVEI 362
            |   | |:  ||| |||  :         |:
Db   257 LIAMLVVLETFCE-LHELKKFRKMFVKKDKDEDQVHIVE-------------------  295

Qy   363 HDKL------QRAATIRSMERR 378
            ||:|     :||::: :::
Db   296 HDQLSFSSITDQAASVKEEQKQ 317
```

```
Search completed: June 29, 2004, 18:19:23
Job time : 47 secs
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OM protein - protein search, using sw model

```
                Copyright  GenCore version 5.1.6
                          (c) 1993 - 2004  Compugen Ltd.

Run on:      June 29, 2004, 18:11:07 ; Search time 59 Seconds
                                (without alignments)
                                2576.450 Million cell updates/sec

Title:       US-09-892-360-2
Perfect score: 2760
Sequence:    2760
         1 MFFLYTDFPLSLVAVPAAAP.........IPTDTKDREPENNSLLEDRN 538
Scoring table: BLOSUM62
         Gapop 10.0 , Gapext 0.5

Searched:    1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters:   1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   A_Geneseq_29Jan04:*
         1: geneseqp1980s:*
         2: geneseqp1990s:*
         3: geneseqp2000s:*
         4: geneseqp2001s:*
         5: geneseqp2002s:*
         6: geneseqp2003as:*
         7: geneseqp2003bs:*
         8: geneseqp2004s:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query Match | Length | DB | ID | ID | Description |
|---|---|---|---|---|---|---|---|
| 1 | 2760 | 100.0 | 538 | 5 | AAB47930 | AAB47930 | Human TRE |
| 2 | 2760 | 100.0 | 538 | 5 | AAE16596 | AAE16596 | Human TWI |
| 3 | 2760 | 100.0 | 538 | 5 | ABP69333 | ABP69333 | Human pol |
| 4 | 2697 | 97.7 | 543 | 5 | AAE21804 | AAE21804 | Human TRE |
| 5 | 2697 | 97.7 | 543 | 5 | AAU81354 | AAU81354 | Novel hum |
| 6 | 2697 | 97.7 | 543 | 5 | AAU79472 | AAU79472 | Human nov |
| 7 | 2697 | 97.7 | 543 | 5 | ABB83542 | ABB83542 | Hypothala |
| 8 | 2697 | 97.7 | 543 | 6 | ADA05746 | ADA05746 | Human NOV |
| 9 | 2697 | 97.7 | 543 | 7 | ADE08315 | ADE08315 | Novel pro |
| 10 | 2693 | 97.6 | 543 | 5 | AAU79473 | AAU79473 | Human nov |
| 11 | 2657.5 | 96.3 | 724 | 5 | AAO14193 | AAO14193 | Human tra |
| 12 | 1630 | 59.1 | 383 | 4 | ABG02731 | ABG02731 | Novel hum |
| 13 | 1412.5 | 51.2 | 557 | 4 | ABG08305 | ABG08305 | Novel hum |
| 14 | 1251.5 | 45.3 | 411 | 3 | AAE10342 | AAE10342 | Murine TR |
| 15 | 1248.5 | 45.2 | 411 | 2 | AAY28497 | AAY28497 | Mouse h-T |
| 16 | 1247 | 45.2 | 370 | 2 | AAY30648 | AAY30648 | A mechani |
| 17 | 1243 | 45.0 | 411 | 3 | AAE10341 | AAE10341 | Human TRE |
| 18 | 1242.5 | 45.0 | 411 | 2 | AAY34133 | AAY34133 | Human pot |
| 19 | 1242.5 | 45.0 | 411 | 2 | AAY28496 | AAY28496 | h-TREK1 p |
| 20 | 1242.5 | 45.0 | 411 | 4 | AAB50044 | AAB50044 | Human TRE |
| 21 | 1235 | 44.7 | 411 | 5 | AAE16597 | AAE16597 | Human TWI |
| 22 | 1218.5 | 44.1 | 426 | 4 | AAU07622 | AAU07622 | Human pot |
| 23 | 1218.5 | 44.1 | 426 | 4 | AAU07618 | AAU07618 | Human pot |
| 24 | 1214.5 | 44.0 | 426 | 4 | AAU07623 | AAU07623 | Human pot |
| 25 | 1210.5 | 43.9 | 426 | 4 | AAU07625 | AAU07625 | Human pot |
| 26 | 1210.5 | 43.9 | 426 | 4 | AAU07624 | AAU07624 | Human pot |
| 27 | 1047 | 37.9 | 337 | 6 | ABR41487 | ABR41487 | Human DIT |
| 28 | 825.5 | 29.9 | 1314 | 4 | AAU04571 | AAU04571 | Human G-p |
| 29 | 825.5 | 29.9 | 1314 | 6 | ABU60872 | ABU60872 | Human G p |
| 30 | 822.5 | 29.8 | 419 | 5 | AAG78406 | AAG78406 | Amino aci |
| 31 | 822.5 | 29.8 | 419 | 7 | AAE38597 | AAE38597 | Human pot |
| 32 | 812.5 | 29.4 | 392 | 6 | ABU60891 | ABU60891 | Human G p |
| 33 | 812.5 | 29.4 | 393 | 3 | AAY94426 | AAY94426 | Human h-T |
| 34 | 812.5 | 29.4 | 393 | 3 | AAY94425 | AAY94425 | Human h-T |
| 35 | 812.5 | 29.4 | 393 | 4 | AAG67777 | AAG67777 | Human mec |
| 36 | 790 | 28.6 | 398 | 2 | AAY30647 | AAY30647 | A mechani |
| 37 | 782 | 28.3 | 398 | 5 | AAE16598 | AAE16598 | Human TWI |
| 38 | 774 | 28.0 | 155 | 4 | AAM24148 | AAM24148 | Human EST |
| 39 | 774 | 28.0 | 155 | 7 | ADE09289 | ADE09289 | Novel pro |
| 40 | 610.5 | 22.1 | 421 | 4 | ABB12229 | ABB12229 | Human K c |
| 41 | 523.5 | 19.0 | 295 | 5 | AAE21164 | AAE21164 | Human TRI |
| 42 | 512 | 18.6 | 294 | 5 | AAU99892 | AAU99892 | Human pot |
| 43 | 512 | 18.6 | 294 | 6 | ABG72802 | ABG72802 | Human 667 |
| 44 | 511 | 18.5 | 292 | 6 | AAU99893 | AAU99893 | Rat potas |
| 45 | 511 | 18.5 | 292 | 5 | AAU99894 | AAU99894 | Mouse pot |

ALIGNMENTS

```
RESULT 1
AAB47930
ID   AAB47930 standard; protein; 538 AA.
XX
AC   AAB47930;
XX
DT   10-JUN-2002  (first entry)
XX
DE   Human TREK2.
XX
KW   Human; K+; channel; potassium; TREK2; pore domain; general anaesthetic;
KW   neurotransmitter receptor.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Domain          72. .90
FT                   /note= "Membrane spanning domain 1"
FT   Domain          152. .175
FT                   /note= "Pore domain 1"
FT   Domain          183. .203
FT                   /note= "Membrane spanning domain 2"
FT   Domain          234. .255
FT                   /note= "Membrane spanning domain 3"
FT   Domain          261. .284
FT                   /note= "Pore domain 2"
FT   Domain          300. .319
FT                   /note= "Membrane spanning domain 4"
XX
PN   WO200200715-A2.
XX
PD   03-JAN-2002.
XX
PF   27-JUN-2001; 2001WO-IB001436.
XX
PR   27-JUN-2000; 2000US-0214559P.
PR   27-JUN-2001; 2001US-00892360.
XX
PA   (CNRS ) CNRS CENT NAT RECH SCI.
XX
PI   Lazdunski M, Lesage F, Romey G;
XX
DR   WPI; 2002-139903/18.
DR   N-PSDB; AAI72558.
XX
PT   New mammalian K+ channel protein with two pore domains, for screening
PT   various compounds, particularly for identifying biologically active
PT   compounds with anesthetic properties.
```

XX
PS   Claim 3; Page 44-46; 50pp; English.
XX
CC   This sequence shows a protein, which constitutes a human K+ channel,
CC   TREK2, which has two pore domains that produces currents whose current-
CC   voltage relationship is slightly inwardly rectifying in high symmetrical
CC   K+ conditions. TREK2 is activated by general anaesthetics at clinical
CC   concentrations. It is modulated by different types of neurotransmitter
CC   receptors. The TREK2 gene produces a cDNA of 2730 bp which contains an
CC   open reading frame of 1617 nucleotides. The TREK2 protein has the same
CC   overall structure as previously described K+ channels. It has four
CC   membrane spanning domains (M1-M4), two pore domains (P1-P2) and an
CC   extended loop between M1 and P1. TREK2 shares 63% identity and 78%
CC   homology to TREK1. The chromosomal location of the TREK2 gene is 14q31.
CC   TREK2 is useful in methods for screening various compounds. In
CC   particular, the protein is useful in methods for identifying biologically
CC   active compounds with anaesthetic properties
XX
SQ   Sequence 538 AA;

Query Match        100.0%;   Score 2760;  DB 5;   Length 538;
Best Local Similarity 100.0%;  Pred. No. 6e-244;
Matches  538;  Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

Qy      1 MFFLYTDFFLSLVAVPAAAPVCQPKSATNGQPPAPAPTPTPRLSISSRATVVARMEGTSQ 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MFFLYTDFFLSLVAVPAAAPVCQPKSATNGQPPAPAPTPTPRLSISSRATVVARMEGTSQ 60

Qy     61 GGLQTVMKWKTVVAIFVVVVVYLVTGGLVFRALEQPFESSQKNTIALEKAEFLRDHVCVS 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 GGLQTVMKWKTVVAIFVVVVVYLVTGGLVFRALEQPFESSQKNTIALEKAEFLRDHVCVS 120

Qy    121 PQELETLIQHALDADNAGVSPIGNSSNNSSHWDLGSAFFFAGTVITTIGYGNIAPSTEGG 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 PQELETLIQHALDADNAGVSPIGNSSNNSSHWDLGSAFFFAGTVITTIGYGNIAPSTEGG 180

Qy    181 KIFCILYAIFGIPLFGFLLAGIGDQLGTIFGKSIARVEKVFRKKQVSQTKIRVISTILFI 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 KIFCILYAIFGIPLFGFLLAGIGDQLGTIFGKSIARVEKVFRKKQVSQTKIRVISTILFI 240

Qy    241 LAGCIVFVTIPAVIFKYIEGWTALESIYFVVVTLTTVGFGDFVAGNAGINYREWYKPLV 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 LAGCIVFVTIPAVIFKYIEGWTALESIYFVVVTLTTVGFGDFVAGNAGINYREWYKPLV 300

Qy    301 WFWILVGLAYFAAVLSMIGDWLRVLSKKTKEEVGEIKAHAAEWKANVTAEFRETRRRLSV 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 WFWILVGLAYFAAVLSMIGDWLRVLSKKTKEEVGEIKAHAAEWKANVTAEFRETRRRLSV 360

Qy    361 EIHDKLQRAATIRSMERRRLGLDQRAHSLDMLSPEKRSVFAALDTGRFKASSQESINNRP 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 EIHDKLQRAATIRSMERRRLGLDQRAHSLDMLSPEKRSVFAALDTGRFKASSQESINNRP 420

Qy    421 NNLRLKGPEQLNKHGQGASEDNIINKFGSTSRLTKRKNKDLKKTLPEDVQKIYKTFRNYS 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 NNLRLKGPEQLNKHGQGASEDNIINKFGSTSRLTKRKNKDLKKTLPEDVQKIYKTFRNYS 480

Qy    481 LDEEKKEETEKMCNSDNSSTAMLTDCIQQHAELENGMIPTDTKDREPENNSLLEDRN 538
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 LDEEKKEETEKMCNSDNSSTAMLTDCIQQHAELENGMIPTDTKDREPENNSLLEDRN 538

RESULT 2
AAE16596
ID   AAE16596 standard; protein; 538 AA.
XX
AC   AAE16596;
XX
DT   18-APR-2002  (first entry)
XX
DE   Human TWIK-Related K+ channel-2 (TREK-2) protein.
XX
KW   Human; TWIK-Related K+ Channel-2; TREK-2; anaesthetic; chromosome 14q31;
KW   screening.

---

XX
OS   Homo sapiens.
XX
FH   Key            Location/Qualifiers
FT   Region         72..90
FT                  /note= "M1 membrane spanning segment"
FT   Domain         152..175
FT                  /note= "P1 pore domain"
FT   Region         183..203
FT                  /note= "M2 membrane spanning segment"
FT   Region         234..255
FT                  /note= "M3 membrane spanning segment"
FT   Domain         261..284
FT                  /note= "P2 pore domain"
FT   Region         300..319
FT                  /note= "M4 membrane spanning segment"
XX
PN   WO200200715-A2.
XX
PD   03-JAN-2002.
XX
PF   27-JUN-2001; 2001WO-IB001436.
XX
PR   27-JUN-2000; 2000US-0214559P.
PR   27-JUN-2001; 2001US-00892360.
XX
PA   (CNRS ) CNRS CENT NAT RECH SCI.
XX
PI   Lazdunski M,  Lesage F,  Romey G;
XX
DR   WPI; 2002-139903/18.
DR   N-PSDB; AAD27459.
XX
PT   New mammalian K+ channel protein with two pore domains, for screening
PT   various compounds, particularly for identifying biologically active
PT   compounds with anaesthetic properties.
XX
PS   Claim 3; Page 45-47; 50pp; English.
XX
CC   The invention relates to a mammalian K+ channel protein with two pore
CC   domains, called TREK2 (TWIK-Related K+ Channel). The protein produces
CC   currents whose current-voltage relationship is slightly inwardly
CC   rectifying in high symmetrical K+ conditions. TREK2 is a member of the
CC   fatty acid-activated and mechanosensitive K+ channel family. TREK-2 gene
CC   located on chromosome 14q31 is abundantly expressed in kidney, pancreas
CC   and moderately in testis, brain, colon and small intestine. The mammalian
CC   K+ channel protein is useful in methods for screening various compounds.
CC   In particular, the protein is useful in methods for identifying compounds
CC   biologically active compounds with anaesthetic properties. The present
CC   sequence is human TREK-2 protein
XX
SQ   Sequence 538 AA;

Query Match        100.0%;   Score 2760;  DB 5;   Length 538;
Best Local Similarity 100.0%;  Pred. No. 6e-244;
Matches  538;  Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

Qy      1 MFFLYTDFFLSLVAVPAAAPVCQPKSATNGQPPAPAPTPTPRLSISSRATVVARMEGTSQ 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MFFLYTDFFLSLVAVPAAAPVCQPKSATNGQPPAPAPTPTPRLSISSRATVVARMEGTSQ 60

Qy     61 GGLQTVMKWKTVVAIFVVVVVYLVTGGLVFRALEQPFESSQKNTIALEKAEFLRDHVCVS 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 GGLQTVMKWKTVVAIFVVVVVYLVTGGLVFRALEQPFESSQKNTIALEKAEFLRDHVCVS 120

Qy    121 PQELETLIQHALDADNAGVSPIGNSSNNSSHWDLGSAFFFAGTVITTIGYGNIAPSTEGG 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 PQELETLIQHALDADNAGVSPIGNSSNNSSHWDLGSAFFFAGTVITTIGYGNIAPSTEGG 180

Qy    181 KIFCILYAIFGIPLFGFLLAGIGDQLGTIFGKSIARVEKVFRKKQVSQTKIRVISTILFI 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 KIFCILYAIFGIPLFGFLLAGIGDQLGTIFGKSIARVEKVFRKKQVSQTKIRVISTILFI 240

```
Qy    241  LAGCIVFVTIPAVIFKYIEGWTALESIYFVVVTLTTVGFGDFVAGGNAGINYREWYKPLV  300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241  LAGCIVFVTIPAVIFKYIEGWTALESIYFVVVTLTTVGFGDFVAGGNAGINYREWYKPLV  300

Qy    301  WFWILVGLAYFAAVLSMIGDWLRVLSKKTKEEVGEIKAHAAEWKANVTAEFRETRRRLSV  360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301  WFWILVGLAYFAAVLSMIGDWLRVLSKKTKEEVGEIKAHAAEWKANVTAEFRETRRRLSV  360

Qy    361  EIHDKLQRAATIRSMERRRLGLDQRAHSLDMLSPEKRSVFAALDTGRFKASSQESINNRP  420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361  EIHDKLQRAATIRSMERRRLGLDQRAHSLDMLSPEKRSVFAALDTGRFKASSQESINNRP  420

Qy    421  NNLRLKGPEQLNKHGQGASEDNIINKFGSTSRLTKRKNDLKKTLPEDVQKIYKTFRNYS  480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421  NNLRLKGPEQLNKHGQGASEDNIINKFGSTSRLTKRKNDLKKTLPEDVQKIYKTFRNYS  480

Qy    481  LDEEKKEEETEKMCNSDNSSTAMLTDCIQQHAELENGMIPTDTKDREPENNSLLEDRN  538
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481  LDEEKKEEETEKMCNSDNSSTAMLTDCIQQHAELENGMIPTDTKDREPENNSLLEDRN  538
```

RESULT 3
ABP69333
ID ABP69333 standard; protein; 538 AA.
XX
AC ABP69333;
XX
DT 20-JAN-2003 (first entry)
XX
DE Human polypeptide SEQ ID NO 1380.
XX
KW Human; genome mapping; gene therapy; food supplement; virus; fungus;
KW cell-proliferative disorder; neurodegenerative disease; bacterial;
KW Parkinson's disease; Alzheimer's disease; autoimmune disease;
KW multiple sclerosis; diabetes; genetic disorder; wound; burn; infection;
KW arthritis; cytostatic; immunomodulator; nootropic; neuroprotective;
KW antiparkinsonian; antidiabetic; immunosuppressive; dermatological;
KW haemostatic; vulnerary; fungicide; antibacterial; virucide; protozoacide;
KW antiarthritic.
XX
OS Homo sapiens.
XX
PN WO200270539-A2.
XX
PD 12-SEP-2002.
XX
PF 05-MAR-2002; 2002WO-US005095.
XX
PR 05-MAR-2001; 2001US-00799451.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Zhou P, Goodrich RW, Asundi V, Zhang J, Zhao QA, Ren F;
PI Xue AJ, Yang Y, Ma Y, Yamazaki V, Chen R, Wang Z, Ghosh M;
PI Wehrman T, Wang J, Wang D, Drmanac RT;
XX
DR WPI; 2002-759812/82.
DR N-PSDB; ABZ11550.
XX
PT New polynucleotides comprising sequences assembled from expressed
PT sequence tags (ESTs), useful for treating cell-proliferative,
PT neurodegenerative, autoimmune, genetic, myeloid or lymphoid, or platelet
PT or coagulation disorders.
XX
PS Claim 9; SEQ ID NO 1380; 1012pp + Sequence Listing; English.
XX
CC The invention relates to an isolated polynucleotide (I) comprising a
CC nucleotide sequence selected from any of 948 sequences (ABZ11119-
CC ABZ12066) or their mature protein coding portion, active domain coding
CC protein or complementary sequences. The polynucleotides are useful for
CC identifying expressed genes or for physical mapping of human genome. The
CC encoded polypeptides (ABP68902-ABP69849) are useful as molecular weight
CC markers, as a food supplement, for generating antibodies, in medical

CC imaging, screening and diagnostic assays and for treating cell-
CC proliferative disorders (cancer), neurodegenerative diseases (Parkinson's
CC or Alzheimer's disease), autoimmune diseases (multiple sclerosis,
CC diabetes, lupus) genetic disorders, myeloid or lymphoid disorders,
CC platelet or coagulation disorders, wound, burns, incision, ulcers, liver
CC or lung fibrosis, infections (bacterial, viral, fungal, parasitic),
CC arthritis, etc. Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 538 AA;

Query Match  100.0%; Score 2760; DB 5; Length 538;
Best Local Similarity 100.0%; Pred. NO. 66-244.;
Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy    1    MFFLYTDFFLSLVAVPAAAPVCQPKSATNGQQPAPAPTPTPRLSISSRATVVARMEGTSQ  60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1    MFFLYTDFFLSLVAVPAAAPVCQPKSATNGQQPAPAPTPTPRLSISSRATVVARMEGTSQ  60

Qy    61   GGLQTVMKWKTVVAIFVVVVYLVTGGLVFRALEQPFESSQKNTIALEKAEFLRDHVCVS  120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61   GGLQTVMKWKTVVAIFVVVVYLVTGGLVFRALEQPFESSQKNTIALEKAEFLRDHVCVS  120

Qy    121  PQELETLIQHALPADNAGVSPIGNSSNNSSHWDLGSAFFAGTVITTIGYGNIAPSTEGG  180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121  PQELSTLIQHALDADNAGVSPIGNSSNNSSHWDLGSAFFAGTVITTIGYGNIAPSTEGG  180

Qy    181  KIFCILYAIFGIPLFGFLLAGIGDQLGTIFGKSIARVEFVFRKKQVSQTKIRVISTILFI  240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181  KIFCILYAIFGIPLFGFLLAGIGDQLGTIFGKSIARVEFVFRKKQVSQTKIRVISTILFI  240

Qy    241  LAGCIVFVTIPAVIFKYIEGWTALESIYFVVVTLTTVGFDFVAGGNAGINYREWYKPLV  300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241  LAGCIVFVTIPAVIFKYIEGWTALESIYFVVVTLTTVGFDFVAGGNAGINYREWYKPLV  300

Qy    301  WFWILVGLAYFAAVLSMIGDWLRVLSKKTKEEVGEIKAHAAEWKANVTAEFRETRRRLSV  360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301  WFWILVGLAYFAAVLSMIGDWLRVLSKKTKEEVGEIKAHAAEWKANVTAEFRETRRRLSV  360

Qy    361  EIHDKLQRAATIRSMERRRLGLDQRAHSLDMLSPEKRSVFAALDTGRFKASSQESINNRP  420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361  EIHDKLQRAATIRSMERRRLGLDQRAHSLDMLSPEKRSVFAALDTGRFKASSQESINNRP  420

Qy    421  NNLRLKGPEQLNKHGQGASEDNIINKFGSTSRLTKRKNDLKKTLPEDVQKIYKTFRNYS  480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421  NNLRLKGPEQLNKHGQGASEDNIINKFGSTSRLTKRKNDLKKTLPEDVQKIYKTFRNYS  480

Qy    481  LDEEKKEEETEKMCNSDNSSTAMLTDCIQQHAELENGMIPTDTKDREPENNSLLEDRN  538
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481  LDEEKKEEETEKMCNSDNSSTAMLTDCIQQHAELENGMIPTDTKDREPENNSLLEDRN  538
```

RESULT 4
AAE21804
ID AAE21804 standard; protein; 543 AA.
XX
AC AAE21804;
XX
DT 16-JUL-2002 (first entry)
XX
DE Human TREK2 protein.
XX
KW Human; hTREK2 protein; cancer; diabetes; pulmonary disease; asthma;
KW cardiovascular disease; inflammatory disease; psychiatric disorder;
KW renal disease; neurodegenerative disease; neurological disorder;
KW Alzheimer's disease; depression; schizophrenia; stroke; vaccine; trauma;
KW pain.
XX
OS Homo sapiens.
XX
PN GB2365010-A.
XX

```
PD   13-FEB-2002.
XX
PF
XX
PR   24-APR-2001; 2001GB-00010129.
XX
PR   25-APR-2000; 2000GB-00010060.
PR   01-JUN-2000; 2000GB-00013370.
XX
PA   (SMIK ) SMITHKLINE BEECHAM CORP.
PA   (SMIK ) SMITHKLINE BEECHAM PLC.
XX
PI   Chapman CG, Duckworth DM;
XX
DR   WPI; 2002-332557/37.
DR   N-PSDB; AAD34451.
XX
PT   Novel human TREK2 (HTREK2) polypeptide and polynucleotide encoding it,
PT   useful for identifying agonists and antagonists in the treatment of
PT   diseases associated with a HTREK2 imbalance, such as diabetes, cancers or
PT   asthma.
XX
PS   Claim 1; Page 21-22; 29pp; English.
XX
CC   The invention relates to human HTREK2 polypeptides and nucleic acid
CC   molecules encoding such polypeptides. TREK2 polypeptides are useful in
CC   screening assays to identify compounds that may stimulate or inhibit
CC   their function or level of expression. Sequences of the invention are
CC   used to treat cancer, diabetes, asthma, pulmonary disease, cardiovascular
CC   diseases, inflammatory disease, renal disease, pain, psychiatric
CC   disorders including depression and schizophrenia, neurodegenerative
CC   disease including Alzheimer's disease, stroke and head trauma and
CC   neurological disorders. They are also used as vaccines. The present
CC   sequence is human hTREK2 protein
XX
SQ   Sequence 543 AA;

Query Match             97.7%;  Score 2697;  DB 5;  Length 543;
Best Local Similarity   100.0%;  Pred. No. 3.6e-238;
Matches   526;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     13 VAVPAAAPVCQPKSAINGQPPAPAPTPTPRLSISSRATVVARMEGTSQGGLQTVMKWKTV 72
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     18 VAVPAAAPVCQPKSAINGQPPAPAPTPTPRLSISSRATVVARMEGTSQGGLQTVMKWKTV 77

Qy     73 VAIFVVVVVYLVTGGLVFRALEQPFESSQKNTIALEKAEFLRDHVCVSPQELETLIQHAL 132
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     78 VAIFVVVVVYLVTGGLVFRALEQPFESSQKNTIALEKAEFLRDHVCVSPQELETLIQHAL 137

Qy    133 DADNAGVSPIGNSSNNSSHWDLGSAFFPAGTVITTIGYGNIAPSTEGGKIFCILYAIFGI 192
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    138 DADNAGVSPIGNSSNNSSHWDLGSAFFPAGTVITTIGYGNIAPSTEGGKIFCILYAIFGI 197

Qy    193 PLFGFLLAGIGDQLGTIFGKSIARVEKVFRRKQVSQTKIRVISTILFILAGCIVFVTIPA 252
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    198 PLFGFLLAGIGDQLGTIFGKSIARVEKVFRRKQVSQTKIRVISTILFILAGCIVFVTIPA 257

Qy    253 VIFKYIEGWTALESIYPVVVLTTVGFGDFVAGGNAGINYREWYKPLVWFWILVGLAYFA 312
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    258 VIFKYIEGWTALESIYPVVVLTTVGFGDFVAGGNAGINYREWYKPLVWFWILVGLAYFA 317

Qy    313 AVLSMIGDWLRVLSKKTKEEVGEIKAHAAEWKANVTAEFRETRRLSVEIHDKLQRAATI 372
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    318 AVLSMIGDWLRVLSKKTKEEVGEIKAHAAEWKANVTAEFRETRRLSVEIHDKLQRAATI 377

Qy    373 RSMERRRLGLDQRAHSLDMLSPEKRSVFAALDTGRFKASSQESINNRPNNLRLKGPEQLN 432
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    378 RSMERRRLGLDQRAHSLDMLSPEKRSVFAALDTGRFKASSQESINNRPNNLRLKGPEQLN 437

Qy    433 KHGQGASEDNIINKFGSTSRLTKRKNKDLKKTLPEDVQKIYKTFRNYSLDEEKKSEETEK 492
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    438 KHGQGASEDNIINKFGSTSRLTKRKNKDLKKTLPEDVQKIYKTFRNYSLDEEKKSEETEK 497

Qy    493 MCNSDNSSTAMLTDCIQQHAELENGMIPTDTKDREPENNSLLEDRN 538
          |||||||||||||||||||||||||||||||||||||||||||||
Db    498 MCNSDNSSTAMLTDCIQQHAELENGMIPTDTKDREPENNSLLEDRN 543
```

```
RESULT 5
AAU81354
ID   AAU81354 standard; protein; 543 AA.
XX
AC   AAU81354;
XX
DT   09-APR-2002 (first entry)
XX
DE   Novel human ion channel protein #34.
XX
KW   Human; ion channel; anti-HIV; analgesic; cytostatic; antidiabetic;
KW   anorectic; metabolic; hypertensive; hypotensive; thrombolytic; cardiant;
KW   antiatherosclerotic; neuroleptic; antimigraine; antiparkinsonian;
KW   tranquiliser; antidepressant; neuroprotective; anticonvulsant; pain;
KW   antiinflammatory; antirheumatic; antiarthritic; immunosuppressive;
KW   antipsoriatic; antiasthmatic; vulnerary; neurological disorder; obesity;
KW   psychiatric disorder; gene therapy; asthma; traumatic brain injury;
KW   human immunodeficiency virus; HIV-1, HIV-2; cancer; diabetes; anorexia;
KW   myocardial infarction; Parkinson's disease; schizophrenia; anxiety;
KW   dementia; Huntington's disease; thyroid disorder; inflammation;
KW   autoimmune disorder; hormonal disorder; renal failure; psoriasis;
KW   movement disorder.
XX
OS   Homo sapiens.
XX
PN   WO200185788-A2.
XX
PD   15-NOV-2001.
XX
PF   10-MAY-2001; 2001WO-US014965.
XX
PR   10-MAY-2000; 2000US-0203305P.
PR   23-MAY-2000; 2000US-0206526P.
PR   25-MAY-2000; 2000US-0207033P.
PR   25-MAY-2000; 2000US-0207092P.
PR   25-MAY-2000; 2000US-0207093P.
PR   07-JUL-2000; 2000US-0216893P.
PR   04-AUG-2000; 2000US-0223245P.
PR   04-OCT-2000; 2000US-0237873P.
XX
PA   (PHAA ) PHARMACIA & UPJOHN CO.
XX
PI   Roberds SL, Benjamin CW, Karnovsky AM, Ruble CL;
XX
DR   WPI; 2002-062237/08.
DR   N-PSDB; ABK27503.
XX
PT   New polynucleotied, useful for identifying ion channel activity
PT   modulators that are used for treating Parkinson's disease, schizophrenia,
PT   migraine, anxiety, manic depression, encodes the ion channel polypeptide.
XX
PS   Claim 2; Page 89; 172pp; English.
XX
CC   The invention relates to an isolated nucleic acid molecule (I) which
CC   encodes a novel ion channel protein, ion-x (II). The nucleic acid,
CC   protein and antibody are useful for identifying a compound which binds a
CC   nucleic acid molecule encoding ion-x. These are useful for treatment of a
CC   neurological or psychiatric disorder which modulates ligand binding to
CC   ion-x in neurons of the mammal; in gene therapy to restore ion-x activity
CC   in certain disease states; for treating asthma, traumatic brain injury,
CC   etc; modulators of ion-x activity or expression are useful for treating
CC   diseases such as viral infections caused by human immunodeficiency virus
CC   (HIV)-1 or HIV-2, pain, cancers, diabetes, obesity, anorexia,
CC   hypertension, hypertension, thrombosis, myocardial infarction,
CC   cardiomyopathies, atherosclerosis, Parkinson's disease, schizophrenia,
CC   migraine, anxiety, manic depression, dementia, Huntington's disease,
CC   thyroid disorders, inflammatory conditions, rheumatoid arthritis,
CC   autoimmune disorders, hormonal disorders, renal failure, psoriasis, and
CC   movement disorders. AAU81321-AAU81360 represent human ion channel protein
CC   sequences of the invention
```

```
XX
SQ   Sequence 543 AA;

Query Match      97.7%;    Score 2697;  DB 5;  Length 543;
Best Local Similarity   100.0%;   Pred. No. 3.6e-238;
Matches 526;   Conservative  0;   Mismatches  0;   Indels  0;   Gaps   0;

Qy    13 VAVPAAAPVCQPKSATNGQPPAPAPTPTPRLSISSRATVVARMEGTSQGGLQTVMKWKTV 72
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    18 VAVPAAAPVCQPKSATNGQPPAPAPTPTPRLSISSRATVVARMEGTSQGGLQTVMKWKTV 77

Qy    73 VAIFVVVVYLVTGGLVFRALEQPFESSQKNTIALEKAEFLRDHVCVSPQELETLIQHAL 132
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    78 VAIFVVVVYLVTGGLVFRALEQPFESSQKNTIALEKAEFLRDHVCVSPQELETLIQHAL 137

Qy   133 DADNAGVSPIGNSSNNSSHWDLGSAFFFAGTVITTIGYGNIAPSTEGGKIFCILYAIFGI 192
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   138 DADNAGVSPIGNSSNNSSHWDLGSAFFFAGTVITTIGYGNIAPSTEGGKIFCILYAIFGI 197

Qy   193 PLFGFLLAGIGDQLGTIFGKSIARVEKVFRKKQVSQTKIRVISTILFILAGCIVFVTIPA 252
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   198 PLFGFLLAGIGDQLGTIFGKSIARVEKVFRKKQVSQTKIRVISTILFILAGCIVFVTIPA 257

Qy   253 VIFKYIEGWTALESIYFVVVTLTTVGFGDFVAGGNAGINYREWYKPLVWFWILVGLAYFA 312
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   258 VIFKYIEGWTALESIYFVVVTLTTVGFGDFVAGGNAGINYREWYKPLVWFWILVGLAYFA 317

Qy   313 AVLSMIGDWLRVLSKKTKEEVGEIKAHAAEWKANVTAEFRETRRRLSVEIHDKLQRAATI 372
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Dby  318 AVLSMIGDWLRVLSKKTKEEVGEIKAHAAEWKANVTAEFRETRRRLSVEIHDKLQRAATI 377

Qy   373 RSMERRRLGLDQRAHSLDMLSPEKRSVFAALDTGRPKASSQESINNRPNNLRLKGPEQLN 432
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   378 RSMERRRLGLDQRAHSLDMLSPEKRSVFAALDTGRPKASSQESINNRPNNLRLKGPEQLN 437

Qy   433 KHGQGASEDNIINKFGSTSRLTKRNKDLKKTLPEDVQKIYKTFRNYSLDEEKKEETEK 492
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   438 KHGQGASEDNIINKFGSTSRLTKRNKDLKKTLPEDVQKIYKTFRNYSLDEEKKEETEK 497

Qy   493 MCNSDNSSTAMLTDCIQQHABLENGMIPTDTKDREPENNSLLEDRN 538
         ||||||||||||||||||||||||||||||||||||||||||||||
Db   498 MCNSDNSSTAMLTDCIQQHABLENGMIPTDTKDREPENNSILEDRN 543
```

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RESULT 6
AAU79472
ID   AAU79472 standard; protein; 543 AA.
XX
AC   AAU79472;
XX
DT   15-JUL-2002   (first entry)
XX
DE   Human novel transporter protein.
XX
KW   Human; transporter; transgenic; transporter mediated disease;
KW   drug screening; pharmacogenomic analysis; chromosome 18.
XX
OS   Homo sapiens.
XX
PN   WO20224748-A2.
XX
PD   28-MAR-2002.
XX
PF   19-SEP-2001; 2001WO-US029211.
XX
PR   19-SEP-2000; 2000US-0233663P.
PR   06-DEC-2000; 2000US-00729920.
XX
PA   (PEKE ) PE CORP NY.
XX
PI   Guegler K, Ketchum KA, Di Francesco V, Beasley EM;
XX
DR   WPI; 2002-351999/38.
```

```
DR   N-PSDB; ABK49585, ABK49586.
XX
PT   New human transporter proteins and nucleic acids, useful as models in the
PT   development of human therapeutic agents, in identifying therapeutic
PT   proteins, or as query sequence in database searches to identify related
PT   sequences.
XX
PS   Claim 1; Fig 2; 207pp; English.
XX
CC   The invention relates to a new isolated peptide being a human transporter
CC   protein, an allelic variant, orthologue, fragment or sequence that is 70%
CC   homologous to the transporter. Also included are a nucleic acid encoding
CC   the transporter (including allelic variants, orthologue, fragment or
CC   complement), an antibody against the protein, a gene chip comprising the
CC   nucleic acids, a transgenic non-human animal comprising the nucleic
CC   acids, a nucleic acid vector comprising the nucleic acids, a host cell
CC   containing the vector, identifying agents that bind to and/or modulate
CC   the function of the transporter, and treating a disease or condition
CC   mediated by a human transporter protein by administering to the patient
CC   an identified agent or modulator. The peptide sequences and the nucleic
CC   acid sequences encoding these peptides can be used as models for the
CC   development of human therapeutic targets, aid in the identification of
CC   therapeutic proteins, and serve as targets for the development of human
CC   therapeutic agents that modulate transporter activity in cells and
CC   tissues that express the transporter. These sequences may also be used as
CC   query sequence in database searches to identify other family members or
CC   related sequences. The proteins may be used to raise antibodies or to
CC   elicit immune response; as a reagent in assays designed to quantitatively
CC   determine protein levels in biological fluids; as markers for tissues in
CC   which the corresponding protein is expressed; in drug screening assays in
CC   cell-based or cell-free systems; to identify compounds that modulate
CC   transporter activity of the protein in its natural state or altered form
CC   that causes a specific disease or pathology associated with the
CC   transporter; as target for diagnosing a disease or predisposition to
CC   disease mediated by the peptide; and in pharmacogenomic analysis. The
CC   nucleic acids are useful as hybridisation probes or primers; in
CC   monitoring the effectiveness of modulating compounds on the expression or
CC   activity of the transporter gene in clinical trials or treatment regimen;
CC   in diagnostic assays for qualitative changes in transporter nucleic acid
CC   expression; and as antisense constructs. The gene for the transporter is
CC   located on chromosome 18. The present sequence represents the novel human
CC   transporter
XX
SQ   Sequence 543 AA;

Query Match      97.7%;    Score 2697;  DB 5;  Length 543;
Best Local Similarity   100.0%;   Pred. No. 3.6e-238;
Matches 526;   Conservative  0;   Mismatches  0;   Indels  0;   Gaps   0;

Qy    13 VAVPAAAPVCQPKSATNGQPPAPAPTPTPRLSISSRATVVARMEGTSQGGLQTVMKWKTV 72
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    18 VAVPAAAPVCQPKSATNGQPPAPAPTPTPRLSISSRATVVARMEGTSQGGLQTVMKWKTV 77

Qy    73 VAIFVVVVYLVTGGLVFRALEQPFESSQKNTIALEKAEFLRDHVCVSPQELETLIQHAL 132
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    78 VAIFVVVVYLVTGGLVFRALEQPFESSQKNTIALEKAEFLRDHVCVSPQELETLIQHAL 137

Qy   133 DADNAGVSPIGNSSNNSSHWDLGSAFFFAGTVITTIGYGNIAPSTEGGKIFCILYAIFGI 192
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   138 DADNAGVSPIGNSSNNSSHWDLGSAFFFAGTVITTIGYGNIAPSTEGGKIFCILYAIFGI 197

Qy   193 PLFGFLLAGIGDQLGTIFGKSIARVEKVFRKKQVSQTKIRVISTILFILAGCIVFVTIPA 252
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   198 PLFGFLLAGIGDQLGTIFGKSIARVEKVFRKKQVSQTKIRVISTILFILAGCIVFVTIPA 257

Qy   253 VIFKYIEGWTALESIYFVVVTLTTVGFGDFVAGGNAGINYREWYKPLVWFWILVGLAYFA 312
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   258 VIFKYIEGWTALESIYFVVVTLTTVGFGDFVAGGNAGINYREWYKPLVWFWILVGLAYFA 317

Qy   313 AVLSMIGDWLRVLSKKTKEEVGEIKAHAAEWKANVTAEFRETRRRLSVEIHDKLQRAATI 372
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   318 AVLSMIGDWLRVLSKKTKEEVGEIKAHAAEWKANVTAEFRETRRRLSVEIHDKLQRAATI 377
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Qy   193  PLFGFLLAGIGDOLGTIFGKSIARVEKVFRKKQVSQTKIRVISTLFILAGCIVFVTIPA  252
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   198  PLFGFLLAGIGDOLGTIFGKSIARVEKVFRKKQVSQTKIRVISTLFILAGCIVFVTIPA  257

Qy   253  VIFKYIEGWTALESIYFVVVTLTTVGFGDFVAGGNAGINYREWYKPLVWFWILVGLAYFA  312
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   258  VIFKYIEGWTALESIYFVVVTLTTVGFGDFVAGGNAGINYREWYKPLVWFWILVGLAYFA  317

Qy   313  AVLSMIGDWLRLVLSKKTKEEVGEIKAHAAEWKANVTAEFRETRRRLSVEIHDKLQRAATI  372
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   318  AVLSMIGDWLRLVLSKKTKEEVGEIKAHAAEWKANVTAEFRETRRRLSVEIHDKLQRAATI  377

Qy   373  RSMERRRLGLDQRAHSLDMLSPEKRSVFAALDTGRFKASSQESINNRPNNLRLKGPEQLN  432
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   378  RSMERRRLGLDQRAHSLDMLSPEKRSVFAALDTGRFKASSQESINNRPNNLRLKGPEQLN  437

Qy   433  KHGQGASEDNIINKFGSTSRLTKRKNKDLKKTLPEDVQKIYKTFRNYSLDEEKKEEETEK  492
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   438  KHGQGASEDNIINKFGSTSRLTKRKNKDLKKTLPEDVQKIYKTFRNYSLDEEKKEEETEK  497

Qy   493  MCNSDNSSTAMLTDCIQQHAELENGMIPTDTKDREPENNSLLEDRN  538
          |||||||||||||||||||||||||||||||||||||||||||||
Db   498  MCNSDNSSTAMLTDCIQQHAELENGMIPTDTKDREPENNSLLEDRN  543
```

RESULT 8
ADA05746
ID   ADA05746 standard; protein; 543 AA.
XX
AC   ADA05746;
XX
DT   06-NOV-2003  (first entry)
XX
DE   Human NOV19a protein SEQ ID NO:106.
XX
KW   human; NOVX; antidiabetic; anorectic; antibacterial; virucide;
KW   immunomodulator; cytostatic; nootropic; neuroprotective;
KW   antiparkinsonian; antilipaemic; gene therapy; human disease;
KW   metabolic disorder; diabetes; obesity; infection; cachexia; cancer;
KW   neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
KW   immune disorder; haematopoietic disorder; dyslipidaemia.
XX
OS   Homo sapiens.
XX
PN   WO2003029424-A2.
XX
PD   10-APR-2003.
XX
PF   02-OCT-2002; 2002WO-US031373.
XX
PR   02-OCT-2001; 2001US-0326483P.
PR   05-OCT-2001; 2001US-0327435P.
PR   05-OCT-2001; 2001US-0327449P.
PR   09-OCT-2001; 2001US-0327917P.
PR   09-OCT-2001; 2001US-0328029P.
PR   09-OCT-2001; 2001US-0328044P.
PR   09-OCT-2001; 2001US-0328056P.
PR   12-OCT-2001; 2001US-0328449P.
PR   15-OCT-2001; 2001US-0329414P.
PR   17-OCT-2001; 2001US-0301142P.
PR   18-OCT-2001; 2001US-0330309P.
PR   22-OCT-2001; 2001US-0341058P.
PR   24-OCT-2001; 2001US-0339266P.
PR   24-OCT-2001; 2001US-0343629P.
PR   29-OCT-2001; 2001US-0349575P.
PR   01-NOV-2001; 2001US-0346357P.
PR   17-APR-2002; 2002US-0373260P.
PR   19-APR-2002; 2002US-0378815P.
PR   19-APR-2002; 2002US-0373817P.
PR   19-APR-2002; 2002US-0373826P.
PR   19-APR-2002; 2002US-0373884P.
PR   22-APR-2002; 2002US-0374977P.
PR   16-MAY-2002; 2002US-0381037P.

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Qy   373  RSMERRRLGLDQRAHSLDMLSPEKRSVFAALDTGRFKASSQESINNRPNNLRLKGPEQLN  432
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   378  RSMERRRLGLDQRAHSLDMLSPEKRSVFAALDTGRFKASSQESINNRPNNLRLKGPEQLN  437

Qy   433  KHGQGASEDNIINKFGSTSRLTKRKNKDLKKTLPEDVQKIYKTFRNYSLDEEKKEEETEK  492
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   438  KHGQGASEDNIINKFGSTSRLTKRKNKDLKKTLPEDVQKIYKTFRNYSLDEEKKEEETEK  497

Qy   493  MCNSDNSSTAMLTDCIQQHAELENGMIPTDTKDREPENNSLLEDRN  538
          |||||||||||||||||||||||||||||||||||||||||||||
Db   498  MCNSDNSSTAMLTDCIQQHAELENGMIPTDTKDREPENNSLLEDRN  543
```

RESULT 7
ABB83542
ID   ABB83542 standard; protein; 543 AA.
XX
AC   ABB83542;
XX
DT   24-SEP-2002  (first entry)
XX
DE   Hypothalamus-expressed potassium channel protein.
XX
KW   Hypothalamus; potassium channel; obesity; human.
XX
OS   Homo sapiens.
XX
PN   WO200252000-A1.
XX
PD   04-JUL-2002.
XX
PF   25-DEC-2001; 2001WO-JP011330.
XX
PR   26-DEC-2000; 2000JP-00396020.
XX
PA   (YAMA ) YAMANOUCHI PHARM CO LTD.
XX
PI   Yokoi H, Inamura K, Sano Y, Miyake A, Mochizuki S;
XX
DR   WPI; 2002-508889/54.
DR   N-PSDB; ABN85879.
XX
PT   Hypothalamus-expressed potassium channel protein and encoded
PT   polynucleotide, applicable in screening inhibitors as anti-obestic agents
PT   to control food intake and enhanced energy consumption.
XX
PS   Claim 1; Page 39-41; 45pp; Japanese.
XX
CC   This invention relates to a hypothalamus-expressed protein having
CC   potassium channel activity. The protein and polynucleotide are applicable
CC   in screening inhibitors as anti-obesity agents to control food intake and
CC   enhanced energy consumption. The said screening process is advantageous
CC   as it is convenient to operate. This sequence represents a potassium
CC   channel activity protein
XX
SQ   Sequence 543 AA;

Query Match        97.7%;     Score 2697;     DB 5;     Length 543;
Best Local Similarity  100.0%;   Pred. No. 3.6e-238;
Matches  526;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;
```

```
Qy    13  VAVPAAAPVCQPKSATNGQPPAPAPTPTPRLSISSRATVVARMEGTSQGGLQTVMKWKTV  72
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    18  VAVPAAAPVCQPKSATNGQPPAPAPTPTPRLSISSRATVVARMEGTSQGGLQTVMKWKTV  77

Qy    73  VAIFVVVVVYLVTGGLVFRALEQPFESSQKNTIALEKAEFLRDHVCVSPQELETLIQHAL  132
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    78  VAIFVVVVVYLVTGGLVFRALEQPFESSQKNTIALEKAEFLRDHVCVSPQELETLIQHAL  137

Qy   133  DADNAGVSPIGNSSNNSSHWDLGSAFFFAGTVITTIGYGNIAPSTEGGKIFCILYAIFGI  192
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   138  DADNAGVSPIGNSSNNSSHWDLGSAFFFAGTVITTIGYGNIAPSTEGGKIFCILYAIFGI  197
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PR   16-MAY-2002;  2002US-0381038P.
PR   16-MAY-2002;  2002US-0381042P.
PR   17-MAY-2002;  2002US-0381642P.
PR   28-MAY-2002;  2002US-0383556P.
PR   29-MAY-2002;  2002US-0383831P.
PR   25-JUN-2002;  2002US-0391135P.
PR   01-OCT-2002;  2002US-00262511.
XX
PA   (CURA-) CURAGEN CORP.
XX
PI   Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X;
PI   Paturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM;
PI   Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton E;
PI   Ji W, Miller CE, Rastelli L, Stone DJ, Pena CEA, Shenoy SG;
PI   Shinkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA;
PI   Eisen AJ, Gangolli EA, Rieger DK, Spaderna SK;
XX
DR   WPI; 2003-381626/36.
DR   N-PSDB; ADA05745.
XX
PT   New NOVX polypeptides and nucleic acids, useful for diagnosing,
PT   preventing or treating NOVX-associated disorders, e.g. diabetes, obesity,
PT   cancer or dyslipidemia, and in chromosome mapping, tissue typing or
PT   pharmacogenomics.
XX
PS   Claim 1; Page 176; 586pp; English.
XX
CC   The present invention describes NOVX proteins, where X can be 1 to 55
CC   (e.g. NOV1). Also described: (1) a composition comprising a polypeptide
CC   described above and a carrier; (2) a kit comprising, in one or more
CC   containers, the composition described above; (3) an isolated nucleic acid
CC   molecule which encodes a NOVX protein of the invention; (4) a vector
CC   comprising the nucleic acid molecule described above; (5) a cell
CC   comprising the above vector; (6) an antibody that immunospecifically
CC   binds to the polypeptide described above; (7) methods for determining the
CC   presence or amount of the above polypeptide or nucleic acid molecule in a
CC   sample; (8) methods for determining the presence of or predisposition to
CC   a disease associated with altered levels of expression of the above
CC   polypeptide or nucleic acid molecule in a first mammalian subject; (9) a
CC   method of identifying an agent that binds to the polypeptide described
CC   above; (10) a method for identifying a potential therapeutic agent for
CC   use in treating a pathology that is related to an aberrant expression or
CC   aberrant physiological interactions of the polypeptide; (11) a method of
CC   screening for a modulator of activity or of latency or predisposition to
CC   a pathology associated with the polypeptide; (12) a method for modulating
CC   the activity of the polypeptide described above; (13) methods of treating
CC   or preventing a pathology associated with the above polypeptide in a
CC   mammal; and (14) a method for producing the above polypeptide. NOVX
CC   sequences have antidiabetic, anorectic, antibacterial, virucide,
CC   immunomodulator, cyrostatic, nootropic, neuroprotective, antiparkinsonian
CC   and antilipaemic activities, and can be used in gene therapy. The
CC   polypeptide is useful in manufacturing a medicament for treating a
CC   syndrome associated with a human disease. The polypeptide or the nucleic
CC   acid molecule may be used to diagnose, treat or prevent metabolic
CC   disorders such as diabetes or obesity; infections; cachexia; cancer;
CC   neurodegenerative disorders such as Alzheimer's disease or Parkinson's
CC   disease; immune disorders; haematopoietic disorders and various
CC   dyslipidaemias. The nucleic acids can also be used as hybridisation
CC   probes, in chromosome mapping, tissue typing; preventive medicine and
CC   pharmacogenomics. The present sequence represents a human NOVX from the
CC   present invention.
XX
SQ   Sequence 543 AA;

Query Match             97.7%;  Score 2697;  DB 6;  Length 543;
Best Local Similarity   100.0%;  Pred. No. 3.6e-238;
Matches  526;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      13 VAVPAAAPVCQPKSATNGQPPAPAPTPTPRLSISSRATVVARMEGTSQGGLQTVMKWKTV 72
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      18 VAVPAAAPVCQPKSATNGQPPAPAPTPTPRLSISSRATVVARMEGTSQGGLQTVMKWKTV 77

Qy      73 VAIFVVVVYLVTGGLVFRALEQPFSSQKNTIALEKAEFLRDHVCVSPQELETLIQHAL 132
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```
Db      78 VAIFVVVVYLVTGGLVFRALEQPFSSQKNTIALEKAEFLRDHVCVSPQELETLIQHAL 137
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     133 DADNAGVSPIGNSSNNSSHWDLGSAFFPAGTVITTIGYGNIAPSTEGGKIFCILYAIFGI 192
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     138 DADNAGVSPIGNSSNNSSHWDLGSAFFPAGTVITTIGYGNIAPSTEGGKIFCILYAIFGI 197
Qy     193 PLFGFLLAGIGDQLGTIFGKSIARVEKVPRKKQVSQTKIRVISTLFILAGCIVFVTIPA 252
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     198 PLFGFLLAGIGDQLGTIFGKSIARVEKVPRKKQVSQTKIRVISTLFILAGCIVFVTIPA 257
Qy     253 VIFKYIEGWTALESIYFVVVTLTTVGFGDFVAGGNAGINYREWYKPLVWFWILVGLAYFA 312
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     258 VIFKYIEGWTALESIYFVVVTLTTVGFGDFVAGGNAGINYREWYKPLVWFWILVGLAYFA 317
Qy     313 AVLSMIGDWLRVLSKKTKBEVGEIKAHAAEWKANVTAEFRETRRLSVEIHDKLQRAATI 372
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     318 AVLSMIGDWLRVLSKKTKBEVGEIKAHAAEWKANVTAEFRETRRLSVEIHDKLQRAATI 377
Qy     373 RSMERRRLGLDQRAHSLDMLSPEKRSVPAALDTGRFKASSQESINNRPNNLRLKGPEQLN 432
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     378 RSMERRRLGLDQRAHSLDMLSPEKRSVPAALDTGRFKASSQESINNRPNNLRLKGPEQLN 437
Qy     433 KHGQGASEDNIINKFGSTSRLTKRQNKDLKKTLPEDVQKIYKTFRNYSLDEEKKEEETEK 492
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     438 KHGQGASEDNIINKFGSTSRLTKRQNKDLKKTLPEDVQKIYKTFRNYSLDEEKKEEETEK 497
Qy     493 MCNSDNSSTAMLTDCIQQHAELENGMIPDTKDREPENNSLLEDRN 538
           |||||||||||||||||||||||||||||||||||||||||||||
Db     498 MCNSDNSSTAMLTDCIQQHAELENGMIPDTKDREPENNSLLEDRN 543


RESULT 9
ADE08315
ID   ADE08315 standard; protein; 543 AA.
XX
AC   ADE08315;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Novel protein (useful for identifying genetic disorders) #470.
XX
KW   novel gene; novel protein; tissue marker; molecular weight marker;
KW   chromosome marker; genetic disorder.
XX
OS   Unidentified.
XX
PN   WO200304152-A2.
XX
PD   03-JUL-2003.
XX
PF   10-DEC-2002;  2002WO-US039555.
XX
PR   10-DEC-2001;  2001US-0339739P.
PR   11-DEC-2001;  2001US-0339453P.
PR   14-MAR-2002;  2002US-0365091P.
PR   14-MAR-2002;  2002US-0365384P.
PR   12-APR-2002;  2002US-0372381P.
PR   12-APR-2002;  2002US-0372615P.
PR   22-APR-2002;  2002US-00128558.
PR   24-APR-2002;  2002US-0376045P.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Tang YT, Asundi V, Goodrich RW, Ren F, Zhang J, Zhao QA, Wang J;
PI   Ghosh M, Xue AJ, Wehrman T, Weng G, Zhou P, Drmanac RT, Wang Z;
PI   Ma Y, Wang D, Chen R, Xu C, Boyle BJ;
XX
DR   WPI; 2003-569235/53.
DR   N-PSDB; ADE07404.
XX
PT   New polynucleotides, useful for expressing recombinant proteins for
PT   analysis, characterization or therapeutic use, or as markers for tissues
```

```
PT                /note= "Wild-type Gln substituted by Lys"
XX
PN   WO20024748-A2.
XX
PD   28-MAR-2002.
XX
PF   19-SEP-2001; 2001WO-US029211.
XX
PR   19-SEP-2000; 2000US-0233663P.
PR   06-DEC-2000; 2000US-00729920.
XX
PA   (PEKE ) PE CORP NY.
XX
PI   Guegler K, Ketchum KA, Di Francesco V, Beasley EM;
XX
DR   WPI; 2002-351999/38.
XX
PT   New human transporter proteins and nucleic acids, useful as models in the
PT   development of human therapeutic agents, in identifying therapeutic
PT   proteins, or as query sequence in database searches to identify related
PT   sequences.
XX
PS   Disclosure; Page; 207pp; English.
XX
CC   The invention relates to a new isolated peptide being a human transporter
CC   protein, an allelic variant, orthologue, fragment or sequence that is 70%
CC   homologous to the transporter. Also included are a nucleic acid encoding
CC   the transporter (including allelic variants, orthologue, fragment or
CC   complement), an antibody against the protein, a gene chip comprising the
CC   nucleic acids, a transgenic non-human animal comprising the nucleic
CC   acids, a nucleic acid vector comprising the nucleic acids, a host cell
CC   containing the vector, identifying agents that bind to and/or modulate
CC   the function of the transporter, and treating a disease or condition
CC   mediated by a human transporter protein by administering to the patient
CC   an identified agent or modulator. The peptide sequences and the nucleic
CC   acid sequences encoding these peptides can be used as models for the
CC   development of human therapeutic targets, aid in the identification of
CC   therapeutic proteins, and serve as targets for the development of human
CC   therapeutic agents that modulate transporter activity in cells and
CC   tissues that express the transporter. These sequences may also be used as
CC   query sequence in database searches to identify other family members or
CC   related sequences. The proteins may be used to raise antibodies or to
CC   elicit immune response; as a reagent in assays designed to quantitatively
CC   determine protein levels in biological fluids; as markers for tissues in
CC   which the corresponding protein is expressed; in drug screening assays in
CC   cell-based or cell-free systems; to identify compounds that modulate
CC   transporter activity of the protein in its natural state or altered form
CC   that causes a specific disease or pathology associated with the
CC   transporter; as target for diagnosing a disease or predisposition to
CC   disease mediated by the peptide; and in pharmacogenomic analysis. The
CC   nucleic acids are useful as hybridisation probes or primers; in
CC   monitoring the effectiveness of modulating compounds on the expression or
CC   activity of the transporter gene in clinical trials or treatment regimen;
CC   in diagnostic assays for qualitative changes in transporter nucleic acid
CC   expression; and as antisense constructs. The gene for the transporter is
CC   located on chromosome 18. The present sequence represents a variant of
CC   the novel human transporter. Note: The present sequence is not shown in
CC   the specification but was created by the indexer from the information in
CC   figure 3 and the transporter sequence appearing as AAU79472
XX
SQ   Sequence 543 AA;

Query Match             97.6%;  Score 2693;  DB 5;  Length 543;
Best Local Similarity   99.8%;  Pred. No. 8.5e-238;
Matches   525;  Conservative    1;  Mismatches   0;  Indels    0;  Gaps    0;

Qy          13 VAVPAAAPVCQPKSATNGQPPAPAPTPTPRLSISSRATVVARMEGTSQGGLQTVMKWKTV 72
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          18 VAVPAAAPVCQPKSATNGQPPAPAPTPTPRLSISSRATVVARMEGTSQGGLQTVMKWKTV 77

Qy          73 VAIFVVVVYLVTGGLVFRALEQPFESSQKNTIALEKAEFLRDHVCVSPQELETLIQHAL 132
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          78 VAIFVVVVYLVTGGLVFRALEQPFESSQKNTIALEKAEFLRDHVCVSPQELETLIQHAL 137
```

```
PT        in which the corresponding protein is preferentially expressed.
XX
PS   Claim 20; SEQ ID NO 1381; 1177pp; English.
XX
CC   The invention comprises the amino acid and coding sequences of novel
CC   proteins. The DNA and protein sequences of the invention are useful as:
CC   markers for tissues in which the corresponding protein is preferentially
CC   expressed; as molecular weight markers on gels; as chromosome markers or
CC   tags; to identify chromosomes or to map related gene positions; and to
CC   compare with endogenous DNA sequences in patients to identify potential
CC   genetic disorders. The present amino acid sequence represents a protein
CC   of the invention.
XX
SQ   Sequence 543 AA;

Query Match             97.7%;  Score 2697;  DB 7;  Length 543;
Best Local Similarity  100.0%;  Pred. No. 3.6e-238;
Matches   526;  Conservative    0;  Mismatches   0;  Indels    0;  Gaps    0;

Qy          13 VAVPAAAPVCQPKSATNGQPPAPAPTPTPRLSISSRATVVARMEGTSQGGLQTVMKWKTV 72
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          18 VAVPAAAPVCQPKSATNGQPPAPAPTPTPRLSISSRATVVARMEGTSQGGLQTVMKWKTV 77

Qy          73 VAIFVVVVYLVTGGLVFRALEQPFESSQKNTIALEKAEFLRDHVCVSPQELETLIQHAL 132
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          78 VAIFVVVVYLVTGGLVFRALEQPFESSQKNTIALEKAEFLRDHVCVSPQELETLIQHAL 137

Qy         133 DADNAGVSPIGNSSNNSSHWDLGSAFFFAGTVITTIGYGNIAPSTEGGKIFCILYAIFGI 192
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         138 DADNAGVSPIGNSSNNSSHWDLGSAFFFAGTVITTIGYGNIAPSTEGGKIFCILYAIFGI 197

Qy         193 PLFGFLLAGIGDQLGTIFGKSIARVEKVFRRKQVSQTKIRVISTILFILAGCIVFVTIPA 252
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         198 PLFGFLLAGIGDQLGTIFGKSIARVEKVFRRKQVSQTKIRVISTILFILAGCIVFVTIPA 257

Qy         253 VIFKYIEGWTALESIYFVVVTLTTVGFGDFVAGGNAGINYREWYKPLVWFWILVGLAYFA 312
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         258 VIFKYIEGWTALESIYFVVVTLTTVGFGDFVAGGNAGINYREWYKPLVWFWILVGLAYFA 317

Qy         313 AVLSMIGDWLRVLSKKTKEEVGEIKAHAAEWKANVTAEFRETRRRLSVEIHDKLQRAATI 372
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         318 AVLSMIGDWLRVLSKKTKEEVGEIKAHAAEWKANVTAEFRETRRRLSVEIHDKLQRAATI 377

Qy         373 RSMERRRLGLDQRAHSLDMLSPEKRSVFAALDTGRFKASSQESINNRPNNLRLKGPEQLN 432
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         378 RSMERRRLGLDQRAHSLDMLSPEKRSVFAALDTGRFKASSQESINNRPNNLRLKGPEQLN 437

Qy         433 KHGQGASEDNIINKFGSTSRLTKRKNKDLKKTLPEDVQKIYKTFRNYSLDEKKEETEK 492
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         438 KHGQGASEDNIINKFGSTSRLTKRKNKDLKKTLPEDVQKIYKTFRNYSLDEKKEETEK 497

Qy         493 MCNSDNSSTAMLTDCIQQHAELENGMIPTDTKDREPENNSLLEDRN 538
               |||||||||||||||||||||||||||||||||||||||||||||
Db         498 MCNSDNSSTAMLTDCIQQHAELENGMIPTDTKDREPENNSLLEDRN 543

RESULT 10
AAU79473
ID   AAU79473 standard; protein; 543 AA.
XX
AC   AAU79473;
XX
DT   15-JUL-2002 (first entry)
XX
DE   Human novel transporter protein variant.
XX
KW   Human; transporter; transgenic; transporter mediated disease;
KW   drug screening; pharmacogenomic analysis; chromosome 18.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 233
```

Qy    133  DADNAGVSPIGNSSNNSSHWDLGSAFFFAGTVITTIGYGNIAPSTEGGKIFCILYAIFGI  192
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    138  DADNAGVSPIGNSSNNSSHWDLGSAFFFAGTVITTIGYGNIAPSTEGGKIFCILYAIFGI  197

Qy    193  PLFGFLLAGIGDQLGTIFGKSIARVEKVFRKKQVSQTKIRVISTILFILAGCIVFVTIPA  252
           |||||||||||||||||||||||||||||||:|||||||||||||||||||||||||||
Db    198  PLFGFLLAGIGDQLGTIFGKSIARVEKVFRKKQVSKTKIRVISTILFILAGCIVFVTIPA  257

Qy    253  VIFKYIEGWTALESIYFVVVTLTTVGFGDFVAGGNAGINYREWYKPLVWFWILVGLAYFA  312
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    258  VIFKYIEGWTALESIYFVVVTLTTVGFGDFVAGGNAGINYREWYKPLVWFWILVGLAYFA  317

Qy    313  AVLSMIGDWLRVLSKKTKEEVGEIKAHAAEWKANVTAEFRETRRLSVEIHDKLQRAATI  372
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    318  AVLSMIGDWLRVLSKKTKEEVGEIKAHAAEWKANVTAEFRETRRLSVEIHDKLQRAATI  377

Qy    373  RSMERRRLGLDQRAHSLDMLSPEKRSVFAALDTGRFKASSQESINNRPNNLRLKGPEQLN  432
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    378  RSMERRRLGLDQRAHSLDMLSPEKRSVFAALDTGRFKASSQESINNRPNNLRLKGPEQLN  437

Qy    433  KHGQGASEDNIINKFGSTSRLTKRKNDLKKTLPEDVQKIYKTFRNYSLDEKKEETEK  492
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    438  KHGQGASEDNIINKFGSTSRLTKRKNDLKKTLPEDVQKIYKTFRNYSLDEKKEETEK  497

Qy    493  MCNSDNSSTAMLTDCIQQHAELENGMIPTDTKDREPENNSLLEDRN  538
           |||||||||||||||||||||||||||||||||||||||||||||
Db    498  MCNSDNSSTAMLTDCIQQHAELENGMIPTDTKDREPENNSLLEDRN  543

RESULT 11
AAO14193
ID   AAO14193  standard; protein; 724 AA.
XX
AC   AAO14193;
XX
DT   03-MAY-2002  (first entry)
XX
DE   Human transporter and ion channel TRICH-10.
XX
KW   Human; transporter and ion channel; TRICH; transport disorder;
KW   neurological disorder; muscle disorder; immunological disorder;
KW   cell proliferative disorder; neuroprotective; nootropic;
KW   cerebroprotective; immunosuppressive; cytostatic; respiratory; muscular;
KW   gene therapy.
XX
OS   Homo sapiens.
XX
PN   WO20020420-A2.
XX
PD   17-JAN-2002.
XX
PF   05-JUL-2001; 2001WO-US021448.
XX
PR   07-JUL-2000; 2000US-0215547P.
PR   14-JUL-2000; 2000US-0218232P.
PR   21-JUL-2000; 2000US-0220112P.
PR   28-JUL-2000; 2000US-0221839P.
XX
PA   (INCY-) INCYTE GENOMICS INC.
XX
PI   Raumann BE, Thornton M, Ding L, Yue H, Tang YT, Harland L;
PI   Burford N, Greene BD, Sanjanwala MS, Baughn MR, Yao MG, Yang J;
PI   Patterson C, Gandhi AR, Hafalia AJA, Tribouley CM, Walia NK;
PI   Au-Young J, Walsh RT, Ramkumar J, Lu Y, Lu DAM, Azimzai Y, Lal P;
PI   Elliott VS, Nguyen DB, Xu Y, Seilhamer JJ, Borowsky ML, Khan FA;
PI   Kearney L, Thangavelu K, Das D, Policky JL;
XX
DR   WPI; 2002-205969/26.
DR   N-PSDB; AAL44676.
XX
PT   New human transporters and ion channel polypeptides for diagnosing,
PT   treating or preventing transport, neurological, muscle, immunological and

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PT   cell proliferative disorders.
XX
PS   Claim 1; Page 158-160; 230pp; English.
XX
CC   The present invention provides the protein and coding sequences of a
CC   number of human transporter and ion channel proteins, designated TRICH-1-
CC   TRICH-32. The sequences can be used in the treatment of transport,
CC   neurological, muscle, immunological and cell proliferative disorders. The
CC   present sequence is a protein of the invention
XX
SQ   Sequence 724 AA;

Query Match             96.3%;  Score 2657.5;  DB 5;  Length 724;
Best Local Similarity   98.7%;  Pred. No. 2.3e-234;
Matches  523;  Conservative  1;  Mismatches  1;  Indels  5;  Gaps  2;

Qy     13  VAVPAAAPVCQPKSATNGQPPAPAPTPTPRLSISSRATVVARMEGTSQGGLQTVMKWKTV  72
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    196  VAVPAAAPVCQPKSATNGQPPAPAPTPTPRLSISSRATVVARMEGTSQGGLQTVMKWKTV  255

Qy     73  VAIFVVVVLVTGGLVFRALEQPPESSQKNTIALEKAEFLRDHVCVSPQELETLIQHAL  132
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    256  VAIFVVVVLVTGGLVFRALEQPPESSQKNTIALEKAEFLRDHVCVSPQELETLIQHAL  315

Qy    133  DADNAGVSPIGNSSNNSSHWDLGSAFFFAGTVITTIGYGNIAPSTEGGKIFCILYAIFGI  192
           ||||||||||||||||||||||||||||||||||||||  ||||||||||||||||||||
Db    316  DADNAGVSPIGNSSNNSSHWDLGSAFFFAGTVITTM-YGNIAPSTEGGKIFCILYAIFGI  374

Qy    193  PLFGFLLAGIGDQLGTIFGKSIARVEKVFRKKQVSQTKIRVISTILFILAGCIVFVTIPA  252
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    375  PLFGFLLAGIGDQLGTIFGKSIARVEKVFRKKQVSQTKIRVISTILFILAGCIVFVTIPA  434

Qy    253  VIFKYIEGWTALESIYFVVVTLTTVGFGDFVA---GGNAGINYREWYKPLVWFWILVGL  308
           ||||||||||||||||||||||||||||||||   ||||||||||||||||||||||||
Db    435  VIFKYIEGWTALESIYFVVVTLTTVGFGDFVAVVVFRGNAGINYREWYKPLVWFWILVGL  494

Qy    309  AYFAAVLSMIGDWLRVLSKKTKEEVGEIKAHAAEWKANVTAEFRETRRLSVEIHDKLQR  368
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    495  AYFAAVLSMIGDWLRVLSKKTKEEVGEIKAHAAEWKANVTAEFRETRRLSVEIHDKLQR  554

Qy    369  AATIRSMERRRLGLDQRAHSLDMLSPEKRSVFAALDTGRFKASSQESINNRPNNLRLKGP  428
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    555  AATIRSMERRRLGLDQRAHSLDMLSPEKRSVFAALDTGRFKASSQESINNRPNNLRLKGP  614

Qy    429  EQLNKHGQGASEDNIINKFGSTSRLTKRKNKDLKKTLPEDVQKIYKTFRNYSLDEEKKEE  488
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    615  EQLNKHGQGASEDNIINKFGSTSRLTKRKNKDLKKTLPEDVQKIYKTFRNYSLDEEKKEE  674

Qy    489  ETEKMCNSDNSSTAMLTDCIQQHAELENGMIPTDTKDREPENNSLLEDRN  538
           |||||||||||||||||||||||||||||||||||||||||||||||||
Db    675  ETEKMCNSDNSSTAMLTDCIQQHAELENGMIPTDTKDREPENNSLLEDRN  724

RESULT 12
ABG02731
ID   ABG02731  standard; protein; 383 AA.
XX
AC   ABG02731;
XX
DT   13-FEB-2002  (first entry)
XX
DE   Novel human diagnostic protein #2722.
XX
KW   Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW   food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS   Homo sapiens.
XX
PN   WO200175067-A2.
XX
PD   11-OCT-2001.
XX
PF   30-MAR-2001; 2001WO-US008631.

```
ID   ABG08305 standard; protein; 557 AA.
XX
AC   ABG08305;
XX
DT   13-FEB-2002  (first entry)
XX
DE   Novel human diagnostic protein #8296.
XX
KW   Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW   food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS   Homo sapiens.
XX
PN   WO200175067-A2.
XX
PD   11-OCT-2001.
XX
PF   30-MAR-2001; 2001WO-US008631.
XX
PR   31-MAR-2000; 2000US-00540217.
PR   23-AUG-2000; 2000US-00649167.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Drmanac RT, Liu C, Tang YT;
XX
DR   WPI; 2001-639362/73.
DR   N-PSDB; AAS72492.
XX
PT   New isolated polynucleotide and encoded polypeptides, useful in
PT   diagnostics, forensics, gene mapping, identification of mutations
PT   responsible for genetic disorders or other traits and to assess
PT   biodiversity.
XX
PS   Claim 20; SEQ ID NO 38664; 103pp; English.
XX
CC   The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC   sequences. (I) is useful as hybridisation probes, polymerase chain
CC   reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC   and in recombinant production of (II). The polynucleotides are also used
CC   in diagnostics as expressed sequence tags for identifying expressed
CC   genes. (I) is useful in gene therapy techniques to restore normal
CC   activity of (II) or to treat disease states involving (II). (II) is
CC   useful for generating antibodies against it, detecting or quantitating a
CC   polypeptide in tissue, as molecular weight markers and as a food
CC   supplement. (II) and its binding partners are useful in medical imaging
CC   of sites expressing (II). (I) and (II) are useful for treating disorders
CC   involving aberrant protein expression or biological activity. The
CC   polypeptide and polynucleotide sequences have applications in
CC   diagnostics, forensics, gene mapping, identification of mutations
CC   responsible for genetic disorders or other traits to assess biodiversity
CC   and to produce other types of data and products dependent on DNA and
CC   amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic
CC   amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic
CC   patent did not appear in the printed specification, but was obtained in
CC   electronic format directly from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 557 AA;

Query Match             51.2%;  Score 1412.5;  DB 4;  Length 557;
Best Local Similarity   72.4%;
  Matches  297;  Conservative    2;  Mismatches   18;  Indels   93;  Gaps    4;

Qy    222 RKKQVSQTKIRVISTILFILAGCIVFVTIPAVIFKYIEGWTALESIYFVVVTLTTVGFGD 281
          :||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    148 QKKQVSQTKIRVISTILFILAGCIVFVTIPAVIFKYIEGWTALESIYFVVVTLTTVGFGD 207

Qy    282 FVAG-------------------GNAGINYREWYKPLVWFWIL------ 305
          |||                                           |
Db    208 FVAAHPSDHLCWVITCKGKYLLPDSPQEKATDFSGVAQKRNEFQKPLIWCWELRSYPTA 267

Qy    306 ------------------------VGLAYFA-AVLSMIGDWLRVLSKKTK 330
```

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XX
PR   31-MAR-2000; 2000US-00540217.
PR   23-AUG-2000; 2000US-00649167.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Drmanac RT, Liu C, Tang YT;
XX
DR   WPI; 2001-639362/73.
DR   N-PSDB; AAS56918.
XX
PT   New isolated polynucleotide and encoded polypeptides, useful in
PT   diagnostics, forensics, gene mapping, identification of mutations
PT   responsible for genetic disorders or other traits and to assess
PT   biodiversity.
XX
PS   Claim 20; SEQ ID NO 33090; 103pp; English.
XX
CC   The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC   sequences. (I) is useful as hybridisation probes, polymerase chain
CC   reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC   and in recombinant production of (II). The polynucleotides are also used
CC   in diagnostics as expressed sequence tags for identifying expressed
CC   genes. (I) is useful in gene therapy techniques to restore normal
CC   activity of (II) or to treat disease states involving (II). (II) is
CC   useful for generating antibodies against it, detecting or quantitating a
CC   polypeptide in tissue, as molecular weight markers and as a food
CC   supplement. (II) and its binding partners are useful in medical imaging
CC   of sites expressing (II). (I) and (II) are useful for treating disorders
CC   involving aberrant protein expression or biological activity. The
CC   polypeptide and polynucleotide sequences have applications in
CC   diagnostics, forensics, gene mapping, identification of mutations
CC   responsible for genetic disorders or other traits to assess biodiversity
CC   and to produce other types of data and products dependent on DNA and
CC   amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic
CC   patent did not appear in the printed specification, but was obtained in
CC   electronic format directly from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 383 AA;

Query Match             59.1%;  Score 1630;  DB 4;  Length 383;
Best Local Similarity  100.0%;  Pred. No. 1.7e-140;
  Matches  317;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    222 RKKQVSQTKIRVISTILFILAGCIVFVTIPAVIFKYIEGWTALESIYFVVVTLTTVGFGD 281
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     67 RKKQVSQTKIRVISTILFILAGCIVFVTIPAVIFKYIEGWTALESIYFVVVTLTTVGFGD 126

Qy    282 FVAGGNAGINYREWYKPLVWFWILVGLAYFAAVLSMIGDWLRVLSKKTKEEVGEIKAHAA 341
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    127 FVAGGNAGINYREWYKPLVWFWILVGLAYFAAVLSMIGDWLRVLSKKTKEEVGEIKAHAA 186

Qy    342 EWKANVTAEFRETRRRLSVEIHDKLQRAATIRSMERRRLGLDQRAHSLDMLSPEKRSVFA 401
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    187 EWKANVTAEFRETRRRLSVEIHDKLQRAATIRSMERRRLGLDQRAHSLDMLSPEKRSVFA 246

Qy    402 ALDTGRFKASSQESINNRPNNLRLKGPEQLNKHGQGASEDNIINKFGSTSRLTKRKNKDL 461
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    247 ALDTGRFKASSQESINNRPNNLRLKGPEQLNKHGQGASEDNIINKFGSTSRLTKRKNKDL 306

Qy    462 KKTLPEDVQKIYKTFRNYSLDEKKEETEKMCNSDNSSTAMLTDCIQQHAELENGMIPT 521
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    307 KKTLPEDVQKIYKTFRNYSLDEKKEETEKMCNSDNSSTAMLTDCIQQHAELENGMIPT 366

Qy    522 DTKDREPENNSLLEDRN 538
          |||||||||||||||||
Db    367 DTKDREPENNSLLEDRN 383

RESULT 13
ABG08305
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```
Db   268  LMQERVXKEKPKAAAPNRRGLGTEKLEFXRXEVAAAVEPHAVLSMIGDWLRVLSKKTK  327

Qy   331  EE--------VGEIKAHAAEWKANVTAEFRETRRRLSVEIHDKLQR  368
Db   328  EEVCRPPLFKSPSNLRLLGVAHHVGEIKAHAAEWKANVTAEFRETRRRLSVEIHDKLQR  387

Qy   369  AATIRSMERRRLGLDQRAHSLDMLSPEKRSVFAALDTGRFKASSQESINNRPNNLRLKGP  428
Db   388  AATIRSMERRRLGLDQRAHSLDMLSPEKRSVFAALDTGRFKASSQESINNRPNNLRLKGP  447

Qy   429  EQLNKHGQGASEDNIINKFGSTSRLTKRKNDLKKTLPEDVQKIYKTFRNYSLDEEKKEE  488
Db   448  EQLNKHGQGASEDNIINKFGSTSRLTKRKNDLKKTLPEDVQKIYKTFRNYSLDEEKKEE  507

Qy   489  ETEKMCNSDNSSTAMLTDCIQQHAELENGMIPTDKDREPENNSLLEDRN  538
Db   508  ETEKMCNSDNSSTAMLTDCIQQHAELENGMIPTDKDREPENNSLLEDRN  557
```

RESULT 14
AAB10342
ID   AAB10342 standard; protein; 411 AA.
XX
AC   AAB10342;
XX
DT   10-DEC-2001 (first entry)
XX
DE   Murine TREK-1 potassium channel protein.
XX
KW   Murine; potassium channel protein; TREK-1; anaesthetic; analgesia;
KW   amnesia.
XX
OS   Mus musculus.
XX
PN   WO200047738-A2.
XX
PD   17-AUG-2000.
XX
PF   11-FEB-2000; 2000WO-IB000226.
XX
PR   12-FEB-1999; 99US-0119727P.
PR   11-FEB-2000; 2000US-00503089.
XX
PA   (CNRS ) CNRS CENT NAT RECH SCI.
XX
PI   Lazdunski M, Honore E, Lesage F, Romey G, Patel AJ;
XX
DR   WPI; 2000-549146/50.
DR   N-PSDB; AAD17497.
XX
PT   Novel nucleic acid encoding a TREK-1 potassium channel protein for
PT   transfecting cells to be used to identify compounds with anesthetic
PT   properties.
XX
PS   Claim 9; Page 32-33; 39pp; English.
XX
CC   The invention relates to human and mouse TREK-1 potassium channel
CC   proteins and their corresponding DNA molecules. TREK-1 nucleic acid is
CC   useful for transfecting cells to induce expression of the TREK-1
CC   potassium channel protein. These cells are then used in assays to
CC   identify compounds which have anaesthetic properties, producing a safe,
CC   reversible state of unconsciousness with concurrent amnesia and analgesia
CC   in a mammal upon inhalation. The present sequence is murine TREK-1
CC   potassium channel protein
XX
SQ   Sequence 411 AA;
XX

Query Match             45.3%;  Score 1251.5; DB 3; Length 411;
Best Local Similarity   64.3%;  Pred. No. 9.7e-106;
Matches  247;  Conservative   54;  Mismatches   66;  Indels   17;  Gaps    5;

Qy    17  AAAPVCQPKSATNGQPPAPAPTPTPRLSISSRATVVA-RMEGTSQGGLQTVMKWKTVVAI  75

```
Db     2  AAPDLLDPKSA--------AQNSKPRLSFSSKPTVLASRVESDS--AINVMKWKTVSTI   50

Qy    76  FVVVVYLVTGGLVFRALEQPFSSQKNTIALEKAEFLRDHVCVSPQELETLICHALDAD  135
Db    51  FLVVVLYLIIGAAVFKALEQPQBISQRTTIVIQKQTFIAQHACVNSTELDELIQQIVAAI  110

Qy   136  NAGVSPIGNSSNNSSHWDLGSAFFPAGTVITTIGYGNIAPSTEGKIFPCILYAIFGIPLF  195
Db   111  NAGIIPLGNSSNQVSHWDLGSSFFPAGTVITTIGFGNISPRTEGKIFCIIYALLGIPLF  170

Qy   196  GFLLAGIGDQLGTIFGKSTARVEKVFRKKQVSQTKIRVISTILFILAGCIVFVTIPAVIF  255
Db   171  GFLLAGVGDQLGTIFGKGIAKVEDTFIKWNVSQTKIRIISTIIFILFGCVLFVALPAVIF  230

Qy   256  KYIEGWTALESIYPVVVLTTVGFGDFVAGGNAGINYREWYKPLVWFWILVGLAYFAAVL  315
Db   231  KHIEGWSALDAIYPVVILTTIGFGDYVAGG-SDIEYLDFYKPVVWFWILVGLAYFAAVL  289

Qy   316  SMIGDWLRVLSKKTKEEVGEIKAHAAEWKANVTAEFRETRRRLSVEIHDKLQRAATIRSM  375
Db   290  SMIGDWLRVISKKTKEEVGEFRAFAAAEWTANVTAEFKETRRRLSVEIYDKFQRATSV---  346

Qy   376  ERRRLGLDQRAHSLDMLSPEKRSV  399
Db   347  -KRKLSAELAGNHNQELTPCRRTL  369
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RESULT 15
AAY28497
ID   AAY28497 standard; protein; 411 AA.
XX
AC   AAY28497;
XX
DT   12-OCT-1999 (first entry)
XX
DE   Mouse h-TREK1 polypeptide.
XX
KW   h-TREK1; two pore potassium channel; inflammatory disease;
KW   chromosome 1q32.
XX
OS   Mus musculus.
XX
PN   WO9937762-A1.
XX
PD   29-JUL-1999.
XX
PF   02-DEC-1998; 98WO-EP007805.
XX
PR   27-JAN-1998; 98EP-003005270.
PR   09-OCT-1998; 98GB-00022135.
XX
PA   (SMIK ) SMITHKLINE BEECHAM PLC.
XX
PI   Meadows HJ, Chapman CG;
XX
DR   WPI; 1999-469126/39.
DR   N-PSDB; AAZ00040.
XX
PT   New two pore potassium channel used for, e.g. treatment of cancer,
PT   pulmonary, cardiovascular and inflammatory diseases.
XX
PS   Claim 3; Page 26; 44pp; English.
XX
CC   This sequence is the mouse h-TREK1 polypeptide, encoded by the h-TREK1
CC   polynucleotide AAZ00040. h-TREK1 is a two pore potassium channel. The
CC   polynucleotide sequence of h-TREK1 can be used to diagnose a disease or
CC   susceptibility to a disease related to expression or activity of h-TREK-1
CC   polypeptides. The methods of diagnosis may be used in the treatment of
CC   diseases including cancer, pulmonary, cardiovascular, and inflammatory
CC   diseases, pain, psychiatric disorders including depression and
CC   schizophrenia, neurodegenerative diseases including Alzheimer's, stroke,
CC   and head trauma and neurological disorders including migraine

XX
SQ   Sequence 411 AA;

Query Match          45.2%;   Score 1248.5;  DB 2;  Length 411;
Best Local Similarity  64.3%;  Pred. No. 1.8e-105;
Matches  247;  Conservative  53;  Mismatches  67;  Indels  17;  Gaps   5;

```
Qy   17  AAAPVCQPKSATNGQPPAPAPTPTPRLSISRATVVA-RMEGTSQGGLQTVMKWKTVVAI   75
             ||  : ||||            ||||:|:|:|:|:|              ||||||||
Db    2  AAPDLLDPKSA------AQNSKPRLSFSSKPTVLASRVESDS---AINVMKWKTVSTI   50

Qy   76  FVVVVVYLVTGGLVFRALEQPFESSQKNTIALEKAEFLRDHVCVSPQELETLIQHALDAD  135
         |:|||:|:|||::|:||||          |::|: : ||  :::             :
Db   51  FLVVVLYLIIGAAVFKALEQPQEISQRTTIVIQKQTFIAQHACVNSTELDELIQQIVAAI  110

Qy  136  NAGVSPIGNSSNNSSHWDLGSAFFFAGTVITTIGYGNIAPSTEGGKIFCILYAIFGIPLF  195
         ||  :: |||:||:|||||||||  ||||||||:||||  ||||||||| : :|||:|||
Db  111  NAGIIPLGNSSNQVSHWDLGSSFFFAGTVITTIGFGNISPRTEGGKIFCIIYALLGIPLF  170

Qy  196  GFLLAGIGDQLGTIFGKSIARVEKVFRKKQVSQTKIRVISTILFILAGCIVFVTIPAVIF  255
         |||||| |||||||||  || ||||:| |||||||||||||:||||||:||: :|||:||
Db  171  GFLLAGVGDQLGTIFGKGIAKVEDTFIKWNVSQTKIRIISTIIFILFGCVLFVALPAVIF  230

Qy  256  KYIEGWTALESIYFVVVTLTTVGFGDFVAGGNAGINYREWYKPLVWFWILVGLAYFAAVL  315
         | |||::|:|::||||:||:|::||||:|||  :  || :|:||:|||||||||||||||
Db  231  KHIEGWSALDAIYFVVITLTTIGFGDYVAGG-SDIEYLDFYKPVVWFWILVGLAYFAAVL  289

Qy  316  SMIGDWLRVLSKKTKEEVGEIKAHAAEWKANVTAEPRETRRLSVEIHDKLQRAATIRSM  375
         |||||||||:|||||||||||  |:|:||||:||  ||||||||||:||  |||:
Db  290  SMIGDWLRVISKKTKEEVGEFRAHAAEWTANVTAEFKETRRLSVEIYDKFQRATSV---  346

Qy  376  ERRRLGLDQRAHSLDMLSPEKRSV  399
         :||::| ||| ::|   || :  |
Db  347  -KRKLSAELAGNHNQELTPCMRTL  369
```

Search completed: June 29, 2004, 18:17:55
Job time : 62 secs

```
                GenCore version 5.1.6
        Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on:    June 29, 2004, 18:11:42 ; Search time 18 Seconds
                                      (without alignments)
                                      1556.319 Million cell updates/sec

Title:          US-09-892-360-2
Perfect score:  2760
Sequence:       1 MFFLYTDFFLSLVAVPAAAP.........IPTDTKDREPENNSLLEDRN 538

Scoring table:  BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched:       141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters:   141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :      SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
```

SUMMARIES

| Result No. | Score | % Match | Query Length | DB | ID | Description |
|---|---|---|---|---|---|---|
| 1 | 2760 | 100.0 | 538 | 1 | CIWA_HUMAN | P57789 homo sapien |
| 2 | 2560.5 | 92.8 | 538 | 1 | CIWA_RAT | Q9Ji84 rattus norv |
| 3 | 1251.5 | 45.3 | 411 | 1 | CIW2_MOUSE | P97438 mus musculu |
| 4 | 1218.5 | 44.1 | 426 | 1 | CIW2_HUMAN | O95069 homo sapien |
| 5 | 812.5 | 29.4 | 393 | 1 | CIW4_HUMAN | Q9nyg8 homo sapien |
| 6 | 790 | 28.6 | 398 | 1 | CIW4_MOUSE | O88434 mus musculu |
| 7 | 512 | 18.6 | 309 | 1 | CIWG_HUMAN | Q96t55 homo sapien |
| 8 | 483 | 17.5 | 499 | 1 | CIW5_HUMAN | O95229 homo sapien |
| 9 | 403 | 14.6 | 336 | 1 | CIW1_HUMAN | O00180 homo sapien |
| 10 | 392 | 14.2 | 332 | 1 | CIWH_HUMAN | Q96t54 homo sapien |
| 11 | 390.5 | 14.1 | 336 | 1 | CIW1_MOUSE | O08581 mus musculu |
| 12 | 352.5 | 12.8 | 409 | 1 | CIW3_MOUSE | O35111 mus musculu |
| 13 | 352.5 | 12.8 | 411 | 1 | CIW3_RAT | O54912 rattus norv |
| 14 | 350.5 | 12.7 | 365 | 1 | CIW9_CAVPO | Q9Ji58 cavia porce |
| 15 | 349.5 | 12.7 | 394 | 1 | CIW3_HUMAN | O14649 homo sapien |
| 16 | 348.5 | 12.6 | 318 | 1 | CIWF_RAT | Q8r5l0 rattus norv |
| 17 | 334 | 12.1 | 374 | 1 | CIW9_HUMAN | O9npc2 homo sapien |
| 18 | 333.5 | 12.1 | 313 | 1 | CIW6_HUMAN | Q9Y257 homo sapien |
| 19 | 329 | 11.9 | 330 | 1 | CIWF_HUMAN | Q9h427 homo sapien |
| 20 | 326 | 11.8 | 1001 | 1 | ORK1_DROME | Q94526 drosophila |
| 21 | 321 | 11.6 | 237 | 1 | CIW9_RAT | Q9es08 rattus norv |
| 22 | 308 | 11.2 | 307 | 1 | CIW8_MOUSE | Q9zti mus musculu |
| 23 | 300.5 | 10.9 | 307 | 1 | CIW7_HUMAN | Q9y2u2 homo sapien |
| 24 | 296.5 | 10.7 | 405 | 1 | CIWD_RAT | Q9ers0 rattus norv |
| 25 | 295.5 | 10.7 | 405 | 1 | CIWD_MOUSE | Q8rip5 mus musculu |
| 26 | 295 | 10.7 | 408 | 1 | CIWD_HUMAN | Q9hbl4 homo sapien |
| 27 | 284 | 10.3 | 430 | 1 | CIWC_RAT | Q9ersl rattus norv |
| 28 | 280.5 | 10.2 | 430 | 1 | CIWC_HUMAN | Q9hbl5 homo sapien |
| 29 | 234 | 8.5 | 320 | 1 | TWK7_CAEEL | P34410 caenorhabdi |
| 30 | 217.5 | 7.9 | 691 | 1 | TOK1_YEAST | P40310 saccharomyc |
| 31 | 153.5 | 5.6 | 246 | 1 | KCO4_ARATH | Q9fwx6 arabidopsis |
| 32 | 153.5 | 5.6 | 436 | 1 | KCO6_ARATH | Q9srv6 arabidopsis |
| 33 | 152 | 5.5 | 408 | 1 | KCO5_ARATH | Q9sz8 arabidopsis |
| 34 | 151.5 | 5.5 | 443 | 1 | KCO2_ARATH | Q9f125 arabidopsis |
| 35 | 140.5 | 5.1 | 363 | 1 | KCO1_ARATH | Q8lbl1 arabidopsis |
| 36 | 136 | 4.9 | 228 | 1 | YWS1_CAEEL | Q10937 caenorhabdi |
| 37 | 127 | 4.6 | 630 | 1 | KCD2_HUMAN | Q9nv8 homo sapien |
| 38 | 127 | 4.6 | 630 | 1 | KCD2_RABIT | P59995 oryctolagus |
| 39 | 126.5 | 4.6 | 989 | 1 | KCH1_HUMAN | O95259 homo sapien |
| 40 | 125 | 4.5 | 630 | 1 | KCD2_MOUSE | Q9z0v2 mus musculu |
| 41 | 123 | 4.5 | 457 | 1 | XYLT_LACBR | O52733 lactobacill |
| 42 | 121.5 | 4.4 | 899 | 1 | YA8D_SCHPO | Q09778 schizosacch |
| 43 | 121 | 4.4 | 630 | 1 | KCD2_RAT | Q63881 rattus norv |
| 44 | 119 | 4.3 | 602 | 1 | CIK5_RAT | P19024 rattus norv |
| 45 | 118.5 | 4.3 | 676 | 1 | CIQ1_HUMAN | P51787 homo sapien |

ALIGNMENTS

```
RESULT 1
CIWA_HUMAN
ID   CIWA_HUMAN   STANDARD;      PRT;    538 AA.
AC   P57789; Q8TDK7; Q8TDK8; Q9HB59;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Potassium channel subfamily K member 10 (Outward rectifying potassium
DE   channel protein TREK-2) (TREK-2 K+ channel subunit).
GN   KCNK10 OR TREK2.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORM A).
RX   MEDLINE=20435789; PubMed=1080510;
RA   Lesage F., Terrenoire C., Romey G., Lazdunski M.;
RT   "Human TREK2, a 2P domain mechano-sensitive K+ channel with multiple
RT   regulations by polyunsaturated fatty acids, lysophospholipids and Gs,
RT   Gi, and Gq protein-coupled receptors.";
RL   J. Physiol. (Lond) 539:657-668(2002).
RN   [2]
RP   SEQUENCE FROM N.A. (ISOFORMS B AND C).
RX   MEDLINE=21896087; PubMed=11897838;
RA   Gu W., Schlichthorl G., Hirsch J.R., Engels H., Karschin C.,
RA   Karschin A., Derst C., Steinlein O.K., Daut J.;
RT   "Expression pattern and functional characteristics of two novel splice
RT   variants of the two-pore-domain potassium channel TREK-2.";
RL   J. Physiol. (Lond) 539:657-668(2002).
-!- FUNCTION: OUTWARD RECTIFYING POTASSIUM CHANNEL. PRODUCES RAPIDLY
    ACTIVATING AND NON-INACTIVATING OUTWARD RECTIFIER K(+) CURRENTS.
    ACTIVATED BY ARACHIDONIC ACID AND OTHER NATURALLY OCCURRING
    UNSATURATED FREE FATTY ACIDS.
-!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
-!- ALTERNATIVE PRODUCTS:
    Event=Alternative splicing; Named isoforms=3;
    Name=A; Synonyms=TREK-2a;
      IsoId=P57789-1; Sequence=Displayed;
    Name=B; Synonyms=TREK-2b;
      IsoId=P57789-2; Sequence=VSP_006697;
    Name=C; Synonyms=TREK-2c;
      IsoId=P57789-3; Sequence=VSP_006698;
-!- TISSUE SPECIFICITY: Abundantly expressed in pancreas and kidney
    and to a lower level in brain, testis, colon, and small intestine.
    Isoform b is strongly expressed in kidney (primarily in the
    proximal tubule) and pancreas, whereas isoform c is abundantly
    expressed in brain.
-!- SIMILARITY: Belongs to the two pore domain potassium channel
    family.
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
-------------------------------------------------------------------
DR   EMBL; AF279890; AAG15191.1; -.
DR   EMBL; AF385399; AAL95705.1; -.
DR   EMBL; AF385400; AAL95706.1; -.
DR   Genew; HGNC:6273; KCNK10.
DR   MIM; 605873; -.
DR   GO; GO:0005267; F:potassium channel activity; TAS.
DR   GO; GO:0006810; P:transport; TAS.
DR   InterPro; IPR003280; K+channel_2pore.
DR   InterPro; IPR001622; K+channel_pore.
DR   InterPro; IPR003976; Trek_channel.
DR   PRINTS; PR01333; 2POREKCHANNEL.
DR   PRINTS; PR01499; TREKCHANNEL.
KW   Transport; Ion transport; Ionic channel; Voltage-gated channel;
KW   Potassium channel; Potassium; Transmembrane; Glycoprotein;
KW   Alternative splicing.
FT   DOMAIN        1     71       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     72     92       POTENTIAL.
FT   DOMAIN      154    180       PORE-FORMING 1 (POTENTIAL).
FT   TRANSMEM    182    202       POTENTIAL.
FT   DOMAIN      203    233       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    234    254       POTENTIAL.
FT   DOMAIN      263    294       PORE-FORMING 2 (POTENTIAL).
FT   TRANSMEM    299    319       POTENTIAL.
FT   DOMAIN      320    538       CYTOPLASMIC (POTENTIAL).
FT   CARBOHYD    144    144       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD    147    147       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD    148    148       N-LINKED (GLCNAC...) (POTENTIAL).
FT   VARSPLIC      1     12       MFFLYTDFFLSL -> MKGDRTEGGCRSDS (in isoform
FT                                B).
FT                                /FTId=VSP_006697.
FT   VARSPLIC      1     12       MFFLYTDFFLSL -> MKFPIETPRKQVNWDPK (in
FT                                isoform C).
FT                                /FTId=VSP_006698.
FT   CONFLICT      1      1       E -> G (IN REF. 2).
SQ   SEQUENCE   538 AA;  59764 MW;  8EA615B08D147FBC CRC64;

Query Match             100.0%;  Score 2760;  DB 1;  Length 538;
Best Local Similarity   100.0%;  Pred. No. 2e-161;
  Matches  538;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    1 MFFLYTDFFLSLVAVPAAAPVCQPKSATNGQPPAPAPTPTPRLSISSRATVVARMEGTSQ 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 MFFLYTDFFLSLVAVPAAAPVCQPKSATNGQPPAPAPTPTPRLSISSRATVVARMEGTSQ 60

Qy   61 GGLQTVMKKTVAIFVVVVVLTVGGLIVFRALEQPESSQKNTIALEKAEFLRDHVCVS 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 GGLQTVMKKTVAIFVVVVVLTVGGLIVFRALEQPESSQKNTIALEKAEFLRDHVCVS 120

Qy  121 PQELETLIQHALDADNAGVSPIGNSSNNSSHWDLGSAFFFAGTVITTIGYGNIAPSTEGG 180
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 PQELETLIQHALDADNAGVSPIGNSSNNSSHWDLGSAFFFAGTVITTIGYGNIAPSTEGG 180

Qy  181 KIFCILYAIFGIPLFGFLLAGIGDQLGTIFGKSIARVEKVFRKKQVSQTKIRVISTILFI 240
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 KIFCILYAIFGIPLFGFLLAGIGDQLGTIFGKSIARVEKVFRKKQVSQTKIRVISTILFI 240

Qy  241 LAGCIVFVTIPAVIFKYIEGWTALESIYFVVVTLTTVGFGDFVAGGNAGINYREWYKPLV 300
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 LAGCIVFVTIPAVIFKYIEGWTALESIYFVVVTLTTVGFGDFVAGGNAGINYREWYKPLV 300

Qy  301 WFFILVGLAYFRAVLSMIGDWLRVLSKKTKEEVGEIKAHAEWKANVTAEFRETRRRLSV 360
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  301 WFFILVGLAYFRAVLSMIGDWLRVLSKKTKEEVGEIKAHAEWKANVTAEFRETRRRLSV 360

Qy  361 EIHDKLQRAATIRSMERRRLGLDQRAHSLDMLSPEKRSVFAALDTGRFKASSQESINNRP 420
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  361 EIHDKLQRAATIRSMERRRLGLDQRAHSLDMLSPEKRSVFAALDTGRFKASSQESINNRP 420

Qy  421 NNLRLKGPEQLNKHGQGASEDNIINKFGSTSRLTKRNKDLKKTLPEDVQKIYKTFRNYS 480
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  421 NNLRLKGPEQLNKHGQGASEDNIINKFGSTSRLTKRNKDLKKTLPEDVQKIYKTFRNYS 480

Qy  481 LDEKKEEFTEKMCNSDNSSTAMLTDCIQQHAELENGMIPTDTKDREPENNSLLEDRN 538
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  481 LDEKKEEFTEKMCNSDNSSTAMLTDCIQQHAELENGMIPTDTKDREPENNSLLEDRN 538

RESULT 2
CIWA_RAT
ID   CIWA_RAT      STANDARD;      PRT;   538 AA.
AC   Q9JIS4;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Potassium channel subfamily K member 10 (Outward rectifying potassium
DE   channel protein TREK-2) (TREK-2 K+ channel subunit).
GN   KCNK10 OR TREK2.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20298807; PubMed=10747911;
RA   Bang H., Kim Y., Kim D.;
RT   "TREK-2, a new member of the mechanosensitive tandem-pore K+ channel
RT   family.";
RL   J. Biol. Chem. 275:17412-17419(2000).
CC   -!- FUNCTION: OUTWARD RECTIFYING POTASSIUM CHANNEL. PRODUCES RAPIDLY
CC       ACTIVATING AND NON-INACTIVATING OUTWARD RECTIFIER K(+) CURRENTS.
CC       ACTIVATED BY ARACHIDONIC ACID AND OTHER NATURALLY OCCURRING
CC       UNSATURATED FREE FATTY ACIDS.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC   -!- TISSUE SPECIFICITY: EXPRESSED MAINLY IN THE CEREBELLUM, SPLEEN,
CC       AND TESTIS.
CC   -!- SIMILARITY: Belongs to the two pore domain potassium channel
CC       family.
CC   -----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   or send an email to license@isb-sib.ch).
CC   -----------------------------------------------------------------------
DR   EMBL; AF196965; AAF75132.1; -.
DR   InterPro; IPR003280; K+channel_2pore.
DR   InterPro; IPR001622; K+channel_pore.
DR   InterPro; IPR003976; Trek_channel.
DR   PRINTS; PR01333; 2POREKCHANNEL.
DR   PRINTS; PR01499; TREKCHANNEL.
KW   Transport; Ion transport; Ionic channel; Voltage-gated channel;
KW   Potassium channel; Potassium; Transmembrane; Glycoprotein (POTENTIAL).
FT   DOMAIN        1     71       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     72     92       POTENTIAL.
FT   DOMAIN      154    180       PORE-FORMING 1 (POTENTIAL).
FT   TRANSMEM    182    202       POTENTIAL.
FT   DOMAIN      203    233       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    234    254       POTENTIAL.
FT   DOMAIN      263    294       PORE-FORMING 2 (POTENTIAL).
FT   TRANSMEM    299    319       POTENTIAL.
FT   DOMAIN      320    538       CYTOPLASMIC (POTENTIAL).
FT   CARBOHYD    144    144       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD    147    147       N-LINKED (GLCNAC...) (POTENTIAL).
SQ   SEQUENCE   538 AA;  59800 MW;  1FF33F0A52B97E4 CRC64;

Query Match             92.8%;   Score 2560.5; DB 1;  Length 538;
Best Local Similarity   95.4%;   Pred. No. 3e-149;
  Matches  503;  Conservative    9;  Mismatches    8;  Indels    7;  Gaps    2;

Qy   13 VAVPAAA-PVCQPKSATNGQPPAPAPTPTPRLSISSRATVVARMEGTSQGLQTVMKWKT 71
         |||||||  ||||||||||||||||||||||||||||||||||||||||||  |||
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Db    18  VAVPAAPPVCQPKSATNGH------HPVPRLSISSRATVVARMEGASQGGLQTVMKWKT   71
          |||   ||||||||       ||||| ||||||||:|||||||||
Qy    72  VVAIFVVVVYLVTGGLVFRALEQPFESSQKNTIALEKAEFLRDHVCVSPQELETLIQHA  131
          ||||||||||||||||||||||||||||||||||||||||||||:|||||||||||||
Db    72  VVAIFVVVVYLVTGGLVFRALEQPFESSQKNTIALEKAEFLRDHICVSPQELETLIQHA  131

Qy   132  LDADNAGVSPIGNSSNNSSHWDLGSAFFFAGTVITTIGYGNIAPSTEGGKIFCILYAIFG  191
          |||||||||:||||||||||||||||||||||||||||||||||||||||||||||||||
Db   132  LDADNAGVSPVGNSSNNSSHWDLGSAFFFAGTVITTIGYGNIAPSTEGGKIFCILYAIFG  191

Qy   192  IPLFGFILAGIGDQLGTIFGKSIARVEKVFRKKQVSQTKIRVISTILFILAGCIVFVTIP  251
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   192  IPLFGFILAGIGDQLGTIFGKSIARVEKVFRKKQVSQTKIRVISTILFILAGCIVFVTIP  251

Qy   252  AVIFKYIEGWTALESIYFVVVTLTTVGFGDFVAGGNAGINYREWYKPLVWFWILVGLAYF  311
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   252  AVIFKYIEGWTALESIYFVVVTLTTVGFGDFVAGGNAGINYREWYKPLVWFWILVGLAYF  311

Qy   312  AAVLSMIGDWLRVLSKKTKEEVGEIKAHAAEWKANVTAEFRETRRRLSVEIHDKLQRAAT  371
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   312  AAVLSMIGDWLRVLSKKTKEEVGEIKAHAAEWKANVTAEFRETRRRLSVEIHDKLQRAAT  371

Qy   372  IRSMERRRLGLDQRAHSLDMLSPEKRSVFRALDTGRFKASSQESINNRPNNLRKGPEQL   431
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   372  IRSMERRRLGLDQRAHSLDMLSPEKRSVFRALDTGRFKASSQESINNRPNNLRKGPEQL   431

Qy   432  NKHGQGASEDNIINKFGSTSRLTKRKNKDLKKTLPEDVQKIYKTFRNYSLDEEKKEBETE  491
          ||||||||||||||||||||:|||||||||||||||||||||||||||||||:|||:||
Db   432  NKHGQGASEDNIINKFGSTSKLTKRKNKDLKKTLPEDVQKIYKTFRNYSLDEEKKEDETE  491

Qy   492  KMCNSDNSSTAMLTDCIQQHAELENGMIPTDTKDREPENNSLLEDRN  538
          ||||||||||||||:||||| ||:||||| |:|||| |||||||||||
Db   492  KMCNSDNSSTAMLTECIQQQAEMENGMVFMDTKDQGLENNSLLEDRN  538
```

RESULT 3
CIW2_MOUSE
ID   CIW2_MOUSE     STANDARD;      PRT;   411 AA.
AC   P97438;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Potassium channel subfamily K member 2 (Outward rectifying potassium
DE   channel protein TREK-1) (Two-pore potassium channel TPKC1) (TREK-1 K+
DE   channel subunit).
GN   KCNK2.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A., FUNCTION, AND TISSUE SPECIFICITY.
RC   TISSUE=Brain;
RX   MEDLINE=97157476; PubMed=9003761;
RA   Fink M., Duprat F., Reyes R., Romey G., Heurteaux C.,
RA   Lazdunski M.;
RT   "Cloning, functional expression and brain localization of a novel
RT   unconventional outward rectifier K+ channel.";
RL   EMBO J. 15:6854-6862(1996).
RN   [2]
RP   REVISIONS.
RC   TISSUE=Brain;
RA   Fink M., Duprat F., Lesage F., Reyes F., Romey G., Heurteaux C.,
RA   Lazdunski M.;
RL   Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   ACTIVATION.
RX   MEDLINE=99254548; PubMed=10321245;
RA   Patel A.J., Honore E., Lesage F., Fink M., Romey G., Lazdunski M.;
RT   "Inhalational anesthetics activate two-pore-domain background K+
RT   channels.";
RL   Nat. Neurosci. 2:422-426(1999).
CC   -!- FUNCTION: OUTWARD RECTIFYING POTASSIUM CHANNEL.

CC   -!- SUBUNIT: Homodimer (Potential).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC   -!- TISSUE SPECIFICITY: HIGH EXPRESSION IN BRAIN AND LUNG. ALSO
CC       DETECTED IN KIDNEY, HEART AND SKELETAL MUSCLE. NOT DETECTED IN
CC       LIVER. IN THE BRAIN, HIGHEST EXPRESSION IN OLFACTORY BULB,
CC       HIPPOCAMPUS AND CEREBELLUM.
CC   -!- MISCELLANEOUS: INHIBITED BY BARIUM. ACTIVATED BY VOLATILE GENERAL
CC       ANAESTHETICS SUCH AS CHLOROFORM, DIETHYL ETHER, HALOTHANE AND
CC       ISOFLURANE.
CC   -!- SIMILARITY: Belongs to the two pore domain potassium channel
CC       family.
CC   --------------------------------------------------------------------------
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; U73488; AAC53005.2; -.
DR   MGD; MGI:109366; Kcnk2.
DR   GO; GO:0008076; C:voltage-gated potassium channel complex; IDA.
DR   GO; GO:0005249; F:voltage-gated potassium channel activity; IDA.
DR   GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IDA.
DR   GO; GO:0006811; P:potassium ion transport; IDA.
DR   InterPro; IPR003280; K-channel_2pore.
DR   InterPro; IPR001622; K-channel_pore.
DR   InterPro; IPR003976; Trek_channel.
DR   PRINTS; PR01333; 2POREKCHANEL.
DR   PRINTS; PR01499; TREKCHANNEL.
KW   Transport; Ion transport; Ionic channel; Voltage-gated channel;
KW   Potassium channel; Potassium; Transmembrane; Glycoprotein.
FT   DOMAIN         1     46       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM      47     67       POTENTIAL.
FT   DOMAIN       129    155       PORE-FORMING 1 (POTENTIAL).
FT   DOMAIN       157    177       POTENTIAL.
FT   DOMAIN       178    207       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     208    228       POTENTIAL.
FT   DOMAIN       238    268       PORE-FORMING 2 (POTENTIAL).
FT   TRANSMEM     273    293       POTENTIAL.
FT   DOMAIN       294    411       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN       378    411       ESSENTIAL FOR CHLOROFORM AND HALOTHANE
FT                                 SENSITIVITY.
FT   DOMAIN       354    411       REQUIRED FOR BASAL CHANNEL ACTIVITY.
FT   CARBOHYD      95     95       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD     119    119       N-LINKED (GLCNAC...) (POTENTIAL).
SQ   SEQUENCE   411 AA;  45297 MW;  8F976DDD103EFA05 CRC64;

Query Match             45.3%;
Best Local Similarity   64.3%;
Matches  247;  Conservative   54;  Mismatches   66;  Indels   17;  Gaps    5;

Score 1251.5;  DB 1;  Length 411;
Pred. No. 1.9e-69;

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Qy    17  AAAPVCQPKSATNGQPPAPAPTPTPRLSISSRATVVA-RMEGTSQGGLQTVMKKTVVAI   75
          ||  |||  ||:||           |||| ||:::    |:||:||||||||||:|||
Db     2  AAPDLLDPKSA--------AQNSKPRLSFSSKPTVLASRVESDS--AINVMKWKTVSTI   50

Qy    76  FVVVVYLVTGGLVFRALEQPFESSQKNTIALEKAEFLRDHVCVSPQELETLIQHALDAD  135
          |:|||:||:||||:|||||| | ||:||| |::| ::|  ||| |||:|:||:|:| :
Db    51  FLVVVLYLIIGAAVFKALEQPQEISQRTTIVIQKQTFIAQHACVNSTELDELIQQIVAAI 110

Qy   136  NAGVSPIGNSSNNSSHWDLGSAFFFAGTVITTIGYGNIAPSTEGGKIFCILYAIFGIPLF  195
          |||  ||| || ||||||||| |||||||||||||:||:| :||||||||:||:||||||
Db   111  NAGIIPLGNSNQVSHWDLGSSFFFAGTVITTIGFGNISPRTEGGKIFCIYALLGIPLF   170

Qy   196  GFLLAGIGDQLGTIFGKSIARVEKVFRKKQVSQTKIRVISTILFILAGCIVFVTIPAVIF  255
          |||||| ||||||||||||:|||: | |  |:||||||::|::|:|| ||:||: ||||||
Db   171  GFLLAGVGDQLGTIFGKGIAKVEDTFIKWNVSQTKIRIISTIIFILFGCVLFVALPAVIF  230

Qy   256  KYIEGWTALESIYFVVVTLTTVGFGDFVAGGNAGINYREYKPLVWFWIIVGLAYFAAVL  315
          |:||||:|| :||||||:|||:|||| ||||  ::| :::||| |||| :||||||||||
Db   231  KHIEGWSALDAIYFVVITLTTIGFGDYVAGG-SDIEYLDFYKPVVWFWILVGLAYFAAVL  289
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Qy   316  SMIGDWLRVLSKKTKEEVGEIKAHAAEWKANVTAEFRETRRRLSVEIHDKLQRAATIRSM  375
               ||||||||| :|||||||||||||:|||||||||||||||||:|||||||||||||
Db   290  SMIGDWLRVISKKTKEEVGEFRAHAAEWTANVTAEFKETRRRLSVEIYDKFQRATSV---  346

Qy   376  ERRRLGLDQRAHSLDMLSPEKRSV  399
               :|: || :|:|:|
Db   347  -KRKLSAELAGNHNQELTPCRRTL  369
```

RESULT 4
CIW2_HUMAN
ID   CIW2_HUMAN     STANDARD;      PRT;   426 AA.
AC   O95069; Q9UNE3;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Potassium channel subfamily K member 2 (Outward rectifying potassium
DE   channel protein TREK-1) (TREK-1 K+ channel subunit) (Two-pore
DE   potassium channel TPKC1).
GN   KCNK2 OR TREK1 OR TREK.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99254548; PubMed=10321245;
RA   Patel A.J., Honore E., Lesage F., Fink M., Romey G., Lazdunski M.;
RT   "Inhalational anesthetics activate two-pore-domain background K+
RT   channels.";
RL   Nat. Neurosci. 2:422-426(1999).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RA   Price L.A., Hellings S.E., Hayashi J.H., Pausch M.H.;
RL   Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: OUTWARD RECTIFYING POTASSIUM CHANNEL.
CC   -!- SUBUNIT: Homodimer (Potential).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC   -!- MISCELLANEOUS: ACTIVATED BY VOLATILE GENERAL ANAESTHETICS SUCH AS
CC       CHLOROFORM, HALOTHANE AND ISOFLURANE.
CC   -!- SIMILARITY: Belongs to the two pore domain potassium channel
CC       family.
CC   -------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   -------------------------------------------------------------
DR   EMBL; AF129399; AAD47569.1; -.
DR   EMBL; AF004711; AAD01203.1; -.
DR   Genew; HGNC:6277; KCNK2.
DR   MIM; 603219; -.
DR   GO; GO:0016020; C:membrane; NAS.
DR   GO; GO:0015271; F:outward rectifier potassium channel activity; NAS.
DR   GO; GO:0006813; P:potassium ion transport; NAS.
DR   InterPro; IPR003280; K+channel_2pore.
DR   InterPro; IPR001622; K+channel_2pore.
DR   InterPro; IPR003976; Trek_channel.
DR   PRINTS; PR01333; 2POREKCHANEL.
DR   PRINTS; PR01499; TREKCHANEL.
KW   Transport; Ion transport; Ionic channel; Voltage-gated channel;
KW   Potassium channel; Potassium; Transmembrane; Glycoprotein.
FT   DOMAIN        1     61       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     62     82       POTENTIAL.
FT   DOMAIN      144    170       PORE-FORMING 1 (POTENTIAL).
FT   TRANSMEM    172    192       POTENTIAL.
FT   DOMAIN      193    223       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    224    244       POTENTIAL.
FT   DOMAIN      253    283       PORE-FORMING 2 (POTENTIAL).
FT   TRANSMEM    288    308       POTENTIAL.
FT   DOMAIN      309    426       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN      378    426       ESSENTIAL FOR CHLOROFORM AND HALOTHANE
FT                                SENSITIVITY (BY SIMILARITY).
FT   DOMAIN      354    426       REQUIRED FOR BASAL CHANNEL ACTIVITY (BY
FT                                SIMILARITY).
FT   CARBOHYD    110    110       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    134    134       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CONFLICT      2     16       MISSING (IN REF. 2).
FT   CONFLICT    309    311       RLV -> DWL (IN REF. 2).
FT   CONFLICT    391    391       S -> N (IN REF. 2).
FT   CONFLICT    411    411       A -> T (IN REF. 2).
SQ   SEQUENCE   426 AA;  47016 MW;  2ABA2335D4009F4E CRC64;

Query Match             44.1%;  Score 1218.5;  DB 1;  Length 426;
Best Local Similarity   62.8%;  Pred. No. 2e-67;
Matches  241;  Conservative   58;  Mismatches   68;  Indels   17;  Gaps    5;

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Qy    17  AAAPVCQPKSATNGQPPAPATPTPRLSISSRATVVA-RMEGTSQGGLQTVMKWKTVVAI   75
              |:||||:||    :||| ||        |||||||||||
Db    17  AAPDLLDPKSA------------AQNSKPRLSFSTKPFVLASRVESDT---TINVMKWTVSTI   65

Qy    76  FVVVVYLVTGGLVFRALEQPFESSQKNTIALEKAEFLRDHVCVSPQELETLIQHALDAD  135
              :|||:||   ::  |:| ||||||   ::|  :  :|| :||:|||
Db    66  FLVVVLYLIIGATVFKALEQPHEISQRTTIVIQKQTFISQHSCVNSTELDELIQQIVAAI  125

Qy   136  NAGVSPIGNSSNNSSHWDLGSAFFFAGTVITTIGYGNIAPSTEGGKIFCILYAIFGIPLF  195
              ||| ||| | |  |||||| :|||||||||||||| ||:||||||  ::|| |||||
Db   126  NAGIIPLGNTSNQISHWDLGSSFFFAGTVITTIGFGNISPRTEGGKIFCIIYALLGIPLF  185

Qy   196  GFLLAGIGDLGTIFGKSIARVEKVFRKKQVSQTKIRVISTILFLLAGCIVFVTIPAVIF  255
              ||||||:|||||||| ||  ||:|||||||||:||| |||||||| :|:  :||:|||
Db   186  GFLLAGVGDLGTIFGKGIAKVEDTFIKNVNSQTKIRIISTIIFILFGCVLFVALPAIIF  245

Qy   256  KYIEGWTALBLSIYFVVVTLTTVGFGDFVAGGNAGINYREWYKPLVWFWILVGLAYFAAVL  315
              |:|||| ||:||:|:|||:||||||||| || ||:||||:|  ||:|||||| ||||||
Db   246  KHIEGWSALDAIYFVVITLTTIGFGDYVAGG-SDIEYLDFYKPVVWFWILVGLAYFAAVL  304

Qy   316  SMIGDWLRVLSKKTKEEVGEIKAHAAEWKANVTAEFRETRRRLSVEIHDKLQRAATIRSM  375
              |||||||||:|||||||||||||:|||||||||||||||||:||||||||||||||||||
Db   305  SMIGRLVRVLSKKTKEEVGEFRAHAAEWTANVTAEFKETRRRLSVEIYDKFQRATSI---  361

Qy   376  ERRRLGLDQRAHSLDMLSPEKRSV  399
              :|: || :|:|:|
Db   362  -KRKLSAELAGNHNQELTPCRRTL  384
```

RESULT 5
CIW4_HUMAN
ID   CIW4_HUMAN     STANDARD;      PRT;   393 AA.
AC   Q9NYG8; Q96T94;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Potassium channel subfamily K member 4 (TWIK-related arachidonic acid-
DE   stimulated potassium channel protein) (TRAAK) (Two pore K+ channel
DE   KT4.1).
GN   KCNK4 OR TRAAK.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORM 1).
RC   TISSUE=Brain;
RX   MEDLINE=20499203; PubMed=11042359;
RA   Chapman C.G., Meadows H.J., Godden R.J., Campbell D.A., Duckworth M.,
RA   Kelsell R.E., Murdock P.R., Randall A.D., Rennie G.I., Gloger I.S.;
RT   "Cloning, localisation and functional expression of a novel human,
RT   cerebellum specific, two pore domain potassium channel.";
RL   Brain Res. Mol. Brain Res. 82:74-83(2000).
RN   [2]
RP   SEQUENCE FROM N.A. (ISOFORM 1).

```
RC   TISSUE=Frontal cortex;
RA   Gray A.T.;
RT   "Assignment of KCNK4 encoding the human potassium channel TRAAK to
RT   chromosome 11.";
RL   Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A. (ISOFORM 1).
RX   MEDLINE=20231699; PubMed=10767409;
RA   Lesage F., Maingret F., Lazdunski M.;
RT   "Cloning and expression of human TRAAK, a polyunsaturated fatty
RT   acids-activated and mechano-sensitive K(+) channel.";
RL   FEBS Lett. 471:137-140(2000).
RN   [4]
RP   SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RX   MEDLINE=22178385; PubMed=12191490;
RA   Ozaita A., Vega-Saenz de Miera E.;
RT   "Cloning of two transcripts, HKT4.1a and HKT4.1b, from the human
RT   two-pore K+ channel gene KCNK4. Chromosomal localization, tissue
RT   distribution and functional expression.";
RL   Brain Res. Mol. Brain Res. 102:18-27(2002).
CC   -!- FUNCTION: VOLTAGE INSENSITIVE, INSTANTANEOUS, OUTWARDLY RECTIFYING
CC       POTASSIUM CHANNEL. OUTWARD RECTIFICATION IS REVERSED AT HIGH
CC       EXTERNAL K+ CONCENTRATIONS (BY SIMILARITY).
CC   -!- SUBUNIT: Homodimer (Potential).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC       Name=1; Synonyms=KT4.1a;
CC         IsoId=Q9NYG8-1; Sequence=Displayed;
CC       Name=2; Synonyms=KT4.1b;
CC         IsoId=Q9NYG8-2; Sequence=VSP_006689;
CC   -!- SIMILARITY: Belongs to the two pore domain potassium channel
CC       family.
CC   --------------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; AF248242; AAG31731.1; -.
DR   EMBL; AF247042; AAF64062.1; ALT_INIT.
DR   EMBL; AF259500; AAK49389.1; -.
DR   EMBL; AF259501; AAK49390.1; -.
DR   Genew; HGNC:6279; KCNK4.
DR   MIM; 605720; -.
DR   GO; GO:0005267; F:potassium channel activity; TAS.
DR   GO; GO:0006813; P:potassium ion transport; TAS.
DR   InterPro; IPR003280; K+channel_2pore.
DR   InterPro; IPR001622; K+channel_pore.
DR   InterPro; IPR008074; TRAAK channel.
DR   PRINTS; PR01333; 2POREKCHANEL.
DR   PRINTS; PR01691; TRAAKCHANNEL.
KW   Transport; Ion transport; Potassium; Transmembrane; Glycoprotein;
KW   Potassium channel; Potassium; Ionic channel; Voltage-gated channel;
KW   Alternative splicing.
FT   DOMAIN        1      3       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM      4     24       POTENTIAL.
FT   DOMAIN       89    113       PORE-FORMING 1 (POTENTIAL).
FT   TRANSMEM    118    138       POTENTIAL.
FT   DOMAIN      139    171       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    172    192       POTENTIAL.
FT   DOMAIN      197    221       PORE-FORMING 2 (POTENTIAL).
FT   DOMAIN      234    254       POTENTIAL.
FT   TRANSMEM    255    393       CYTOPLASMIC (POTENTIAL).
FT   CARBOHYD     78     78       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD     82     82       N-LINKED (GLCNAC...) (POTENTIAL).
FT   VARSPLIC      1      1       M -> MTTAPQEPPARPLQAGSGAGPAPGRAM (in
FT                                isoform 2).
FT                                /FTId=VSP_006689.
FT   CONFLICT    328    328       P -> L (IN REF. 2).
```

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SQ   SEQUENCE   393 AA;  42704 MW;  7F18E53A0A9AD57D CRC64;

Query Match             29.4%;  Score 812.5;  DB 1;  Length 393;
Best Local Similarity   53.8%;  Pred. No. 1.1e-42;
Matches  157; Conservative  53; Mismatches  77; Indels  5; Gaps  3;

Qy    67 MKWKTVVAIFVVVVYLVTGGLVFRALEQPFESSQKNTIALEKAEFLRDHVCVSPQELET 126
         |:.||::||:|||||:|||||||||||:.|:||||::. :.:|||||||||||||||||
Db     1 MRSTTILALLALVLLYLVSGALVFRALEQPHEQQAQRELGEVREKFLRAHPCVSDQELGL 60

Qy   127 LIQHALDADNAGVSPIGNSSNNSSH--WDLGSAFFPAGTVITTIGYGNIAPSTEGGKIFC 184
         ||:|.|.||.:||.||:||||||||  |||||||||||||||||||||:|:.:|:
Db    61 LIKEVADALGGGADPETNSTSNSSHSAWDLGSAFFFSGTIITTIGYGNVALRTDAGRLFC 120

Qy   185 ILYAIFGIPLFGFLLAGIGDQLGTIFGKSIARVEKVFRKKQVSQTKIRVISTILFILAGC 244
         |||:||||||:||||:.|||:|: :|:|: .:|::||||.||:||:|:|:.|||:|||||
Db   121 IFYALVGIPLFGILLAGVGDRLGSSLRHGIGHIEAIFLKWHVPPELVRVLSAMLFLLIGC 180

Qy   245 IVFVTIPAVIFKYIEGWTALESIYFVVVITLTTVGFGDFVAGGNAGINYREWYKPLVWFWI 304
         :||||||||||||||||||||::|:|:||||||||||||||||||||||:||||||||||
Db   181 LLFVLTPTFVFCYMEDWSKLEAIYFVIVILTTVGFGDYVAGADPRQD-SPAYQPLVWFWI 239

Qy   305 LVGLAYFAAVLSMIGDWLRVLSKKTKEEVGEIKAHAAEWKANVTAEFRETRR 356
         |:|||||||:.:|||:.|||:|:.:|.:|:.||:|||:.|||
Db   240 LLGLAYFASVLTTIGNWLRVVSRRTRAEMGGLTAQAASWTGTVTA--RVTQR 289
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```
RESULT 6
CIW4_MOUSE
ID   CIW4_MOUSE             STANDARD;      PRT;   398 AA.
AC   O88454;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Potassium channel subfamily K member 4 (TWIK-related arachidonic acid-
DE   stimulated potassium channel protein) (TRAAK).
GN   KCNK4 OR TRAAK.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=9925448; PubMed=9628867;
RA   Fink M., Lesage F., Duprat F., Heurteaux C., Reyes R., Fosset M.,
RA   Lazdunski M.;
RT   "A neuronal two P domain K+ channel stimulated by arachidonic acid and
RT   polyunsaturated fatty acids.";
RL   EMBO J. 17:3297-3308(1998).
RN   [2]
RP   ACTIVATION.
RX   MEDLINE=9925448; PubMed=10321245;
RA   Patel A.J., Honore E., Lesage F., Fink M., Romey G., Lazdunski M.;
RT   "Inhalational anesthetics activate two-pore-domain background K+
RT   channels.";
RL   Nat. Neurosci. 2:422-426(1999).
CC   -!- FUNCTION: VOLTAGE INSENSITIVE, INSTANTANEOUS, OUTWARDLY RECTIFYING
CC       POTASSIUM CHANNEL. OUTWARD RECTIFICATION IS REVERSED AT HIGH
CC       EXTERNAL K+ CONCENTRATIONS.
CC   -!- SUBUNIT: Homodimer (Potential).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC       Name=1;
CC         IsoId=O88454-1; Sequence=Displayed;
CC       Name=2; Synonyms=TRAAKT, Truncated;
CC         IsoId=O88454-2; Sequence=VSP_006690, VSP_006691;
CC   -!- TISSUE SPECIFICITY: EXPRESSED IN BRAIN, SPINAL CORD AND EYE. NOT
CC       DETECTED IN HEART, SKELETAL MUSCLE, LIVER, LUNGS, KIDNEY AND
CC       TESTIS.
CC   -!- MISCELLANEOUS: ACTIVATED BY ARACHIDONIC ACID AND OTHER UNSATURATED
CC       FATTY ACIDS. NOT AFFECTED BY VOLATILE GENERAL ANAESTHETICS SUCH AS
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CC       CHLOROFORM, DIETHYL ETHER, HALOTHANE AND ISOFLURANE.
CC   -!- SIMILARITY: Belongs to the two pore domain potassium channel
CC       family.
CC   --------------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; AF056492; AAC40181.1; -.
DR   MGD; MGI:1298234; Kcnk4.
DR   InterPro; IPR003280; K+channel_2pore.
DR   InterPro; IPR001622; K+channel_pore.
DR   InterPro; IPR0080074; TRAAK_channel.
DR   PRINTS; PR01333; 2POREKCHANNEL.
DR   PRINTS; PR01691; TRAAKCHANNEL.
KW   Transport; Ion transport; Ionic channel; Voltage-gated channel;
KW   Potassium channel; Potassium; Transmembrane; Glycoprotein;
KW   Alternative splicing.
FT   DOMAIN        1      3       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM      4     24       POTENTIAL.
FT   DOMAIN       89    113       PORE-FORMING 1 (POTENTIAL).
FT   TRANSMEM    119    139       POTENTIAL.
FT   DOMAIN      140    171       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    172    192       POTENTIAL.
FT   DOMAIN      198    222       PORE-FORMING 2 (POTENTIAL).
FT   TRANSMEM    235    255       POTENTIAL.
FT   DOMAIN      256    398       CYTOPLASMIC (POTENTIAL).
FT   CARBOHYD     81     81       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD     84     84       N-LINKED (GLCNAC...) (POTENTIAL).
FT   VARSPLIC     63     67       KLIVE -> KAMAI (in isoform 2).
FT                                /FTId=VSP_006690.
FT   VARSPLIC     68    398       Missing (In isoform 2).
FT                                /FTId=VSP_006691.
SQ   SEQUENCE   398 AA;  43051 MW;  478A834B7B7AEC92 CRC64;

     Query Match             28.6%;  Score 790;  DB 1;  Length 398;
     Best Local Similarity   51.9%;  Pred. No. 2.7e-41;
     Matches  152;  Conservative   55;  Mismatches   80;  Indels    6;  Gaps    3;

Qy         67 MKWKTVVAIFVVVVVYLVTGGLVFRALEQPFESSQKNTIALEKAEFLRDHVCVSPQELET 126
              |:|::|:|||:::|||:|||||  :: | | |||:||:||||:||||  ||||| ||||
Db          1 MRSTTLLALLALVLLYLVSGALVFQALEQPHEQQAQKKMDHGRDQFLRDHPCVSQKSLED 60

Qy        127 LIQHALPADNAGVSP---IGNSSNNSSHWDLGSAFFPAGTVITTIGYGNIAPSTEGGKIF 183
                 ::|   |  |    |||::|||:|  ||||||  :||  ||:|||||||:   |||
Db         61 FIKLLVELLGGGANPETSWTNSSNHSSAWNLGGSAFFFSGTIITTIGYGNIVLHTDAGRLF 120

Qy        184 CILYAIFGIPLFGFLLAGIGDQLGTIFGKSIARVEKVFRKKQVSQTKIRVISTILFILAG 243
              ||:| ||||||||||||:|||:|| |   :: | |:| |: :::  :  ||:|||:| :|
Db        121 CIFYALVGIPLFGMLLAGVGDRLGSSLRRGICHIEAIFLKWHVPPGLVRSLSAVLFLLIG 180

Qy        244 CIVFVTIPAVIFKYIEGWTALESIYFVVVTLLTVGFGDFVAGNAGINYREWYKPLVWFW 303
              ||| || |  :|||  ||| :|:|:| :|:|||||:|||:| | |:|| |||:||:|||
Db        181 CLLFVLTPTFVFSYMESWSKLEAIYFVIVTLLTTVGFGDYVPGDGTGQN-SPAYQPLVWFW 239

Qy        304 ILVGLAYFAAVLSMIGDWLRVLSKKTKEEVGEIKAHAAEWKANVTAEFRETRR 356
              |||| || ::|:|:|| |||:| ::|::::: |  :| |:  :|  :|||
Db        240 ILFGLAYFASVLTTIGNWLRAVSRRTRAEMGGLITAQAASWTGTVTA--RVTQR 290


RESULT 7
CIWG_HUMAN
ID   CIWG_HUMAN    STANDARD;    PRT;    309 AA.
AC   Q96T55; Q9H591;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Potassium channel subfamily K member 16 (TWIK-related alkaline pH
DE   activated K+ channel 1) (2P domain potassium channel Talk-1).
GN   KCNK16 OR TALK1.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORM 1).
RC   TISSUE=Pancreas;
RX   MEDLINE=21164727; PubMed=11263999;
RA   Girard C., Duprat F., Terrenoire C., Tinel N., Fosset M., Romey G.,
RA   Lazdunski M., Lesage F.;
RT   "Genomic and functional characteristics of novel human pancreatic 2P
RT   domain K(+) channels.";
RL   Biochem. Biophys. Res. Commun. 282:249-256(2001).
RN   [2]
RP   SEQUENCE FROM N.A. (ISOFORM 2).
RA   Williams S.;
RL   Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Outward rectifying potassium channel. Produces rapidly
CC       activating and non-inactivating outward rectifier K(+) currents.
CC   -!- SUBUNIT: Homodimer (Potential).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC       Name=1;
CC         IsoId=Q96T55-1; Sequence=Displayed;
CC       Name=2;
CC         IsoId=Q96T55-2; Sequence=VSP_006699;
CC         Note=No experimental confirmation available;
CC   -!- TISSUE SPECIFICITY: Highly expressed in pancreas..Not detectable
CC       in the other tissues tested.
CC   -!- MISCELLANEOUS: Inhibited by Ba(+2), quinine, quinidine, chloroform
CC       and halothane. Activated at alkaline pH.
CC   -!- SIMILARITY: Belongs to the two pore domain potassium channel
CC       family.
CC   --------------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; AF358909; AAK49532.1; -.
DR   EMBL; AL136087; CAC07336.1; -.
DR   Genew; HGNC:14464; KCNK16.
DR   MIM; 607369; -.
DR   InterPro; IPR003280; K+channel_2pore.
DR   InterPro; IPR001622; K+channel_pore.
DR   InterPro; IPR003092; TASK_channel.
DR   PRINTS; PR01333; 2POREKCHANNEL.
DR   PRINTS; PR01095; TASKCHANNEL.
KW   Transport; Ion transport; Ionic channel; Voltage-gated channel;
KW   Potassium channel; Potassium; Transmembrane; Alternative splicing.
FT   DOMAIN        1     13       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     14     34       POTENTIAL.
FT   DOMAIN       98    116       PORE-FORMING 1 (POTENTIAL).
FT   TRANSMEM    120    140       POTENTIAL.
FT   DOMAIN      141    165       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    166    186       POTENTIAL.
FT   DOMAIN      202    221       PORE-FORMING 2 (POTENTIAL).
FT   TRANSMEM    238    258       POTENTIAL.
FT   DOMAIN      259    309       CYTOPLASMIC (POTENTIAL)
FT   VARSPLIC    269    309       LRQGCGAKAAPGRRPRRGSTAARGVQVTPQDFPISKKGLGS
FT                                -> RGLGVKDGAASDPSGLPRPQKIPISA (in isoform
FT                                2).
FT                                /FTId=VSP_006699.
SQ   SEQUENCE   309 AA;  34153 MW;  99C4B1EB26B0764 CRC64;

     Query Match             18.6%;  Score 512;  DB 1;  Length 309;
     Best Local Similarity   40.2%;  Pred. No. 1.9e-24;
     Matches   99;  Conservative   55;  Mismatches   86;  Indels    6;  Gaps    3;
```

Qy   72  VVAIFVVVVVYLVTGGLVFRALEQPFESSQKNTIALEKAEFLRDHVCVSPQELETLIQHA 131
         |::::|:|:|| :. :;|:|:: |:. :|: |: . ||:: ||:
Db   14  VLPLLLAYVCYLLLGATIFQLLEROAEAQSRDQFQLEKLRFLENYTCLLDQWAMBQFVQVI 73

Qy  132  LDADNAGVSPIGNSSNNSSHWDLGSAFFFAGTVITTIGYGNIAPSTEGGKIFCILYAIFG 191
         ::|   || ||:| |||:|||||||||||||| |:|:||:. ||:|
Db   74  MEAWYKGVNPKGNST-NPSSNWDFGSSFFFAGTVVTTIGYGNLAPSTEAGQVFCVFYALLG 132

Qy  192  IPLFGFLLAGIGDQLGTIFGKSIARVEKVFRKKQVSQTKIRVISTILFILAGCIVFVTIP 251
         |||  || | . :| ||   :|: |: ||: ||:.:|::|
Db  133  IPLNVIFL---NHLGTGLRAHLAAIERWEDRPRRSQV-LQVLGLALFLTLGTLVILIFP 187

Qy  252  AVIFKYIEGWTALESIYFVVVTLTTVGFGDFVAGGNAGINYREWYKPLVWFWILVGLAYF 311
         :: ||:  |||||:| ||:|::|||||||| ||:.|:::|| :|::|||:
Db  188  PMVFSHVEGWSFSEGFYFAFITLSTIGFGDYVVGTDPSKHYISVVRSLAAIWILLGLAWL 247

Qy  312  AAVLSM 317
         |:|
Db  248  ALILPL 253

RESULT 8
CIW5_HUMAN
ID   CIW5_HUMAN     STANDARD;      PRT;     499 AA.
AC   O95279;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Potassium channel subfamily K member 5 (Acid-sensitive potassium
DE   channel protein TASK-2) (TWIK-related acid-sensitive K+ channel 2).
GN   KCNK5 OR TASK2.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Kidney;
RX   MEDLINE=99030343; PubMed=9812978;
RA   Reyes R., Duprat F., Lesage F., Fink M., Salinas M., Farman N.,
RA   Lazdunski M.;
RT   "Cloning and expression of a novel pH-sensitive two pore domain K+
RT   channel from human kidney.";
RL   J. Biol. Chem. 273:30863-30869(1998).
CC   -!- FUNCTION: PH DEPENDENT, VOLTAGE INSENSITIVE, OUTWARDLY RECTIFYING
CC       POTASSIUM CHANNEL. OUTWARD RECTIFICATION IS LOST AT HIGH EXTERNAL
CC       K+ CONCENTRATIONS.
CC   -!- SUBUNIT: Homodimer (Potential).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC   -!- TISSUE SPECIFICITY: ABUNDANT EXPRESSION IN KIDNEY. ALSO DETECTED
CC       IN LIVER, PLACENTA AND SMALL INTESTINE. IN THE KIDNEY, EXPRESSION
CC       IS RESTRICTED TO THE DISTAL TUBULES AND COLLECTING DUCTS. NOT
CC       EXPRESSED IN PROXIMAL TUBULES OR GLOMERULI.
CC   -!- MISCELLANEOUS: INHIBITED BY QUININE, QUINIDINE AND EXTERNAL
CC       ACIDIFICATION.
CC   -!- SIMILARITY: Belongs to the two pore domain potassium channel
CC       family.
DR   EMBL; AF084830; AAC79458.1; -.
DR   Genew; HGNC:6280; KCNK5.
DR   MIM; 603493;
DR   GO; GO:0005887; C:integral to plasma membrane; TAS.
DR   GO; GO:0005267; F:potassium channel activity; TAS.
DR   GO; GO:0007588; P:excretion; TAS.

DR   GO; GO:0006813; P:potassium ion transport; TAS.
DR   InterPro; IPR003280; K+channel_2pore.
DR   InterPro; IPR001622; K+channel_pore.
DR   InterPro; IPR003092; TASK_channel.
DR   PRINTS; PR01333; 2POREKCHANEL.
DR   PRINTS; PR01095; TASKCHANNEL.
KW   Transport; ion transport; Ionic channel; Voltage-gated channel;
KW   Potassium channel; transmembrane; Glycoprotein.
FT   DOMAIN       1      7       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     8     26       POTENTIAL.
FT   DOMAIN      85    112       PORE-FORMING 1 (POTENTIAL).
FT   TRANSMEM   113    133       POTENTIAL.
FT   DOMAIN     134    157       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM   158    180       POTENTIAL.
FT   DOMAIN     190    215       PORE-FORMING 2 (POTENTIAL).
FT   TRANSMEM   230    250       POTENTIAL.
FT   DOMAIN     251    325       CYTOPLASMIC (POTENTIAL)
FT   CARBOHYD    77     77       N-LINKED (GLCNAC...) (POTENTIAL).
SQ   SEQUENCE   499 AA;  55130 MW;  E871A7A4823DDA00 CRC64;

Query Match             17.5%;  Score 483; DB 1; Length 499;
Best Local Similarity   25.8%;  Pred. No. 2e-22;
Matches 131;  Conservative   81; Mismatches 185; Indels 110; Gaps 14;

Qy   79  VVVYLVTGGLVFRALEQPFESSQKNTIALEKAEFLRDHVCVSPQELETLIQHALDADNAG 138
         :: ||| |:|| |:|:|||||||||||||||||||| |:|:|||
Db   12  IIFYLAIGAAIFEVLEEPHWKEAKKNYYTQKLHLLKEFPCLGQEGLDKILEVVSDAAGQG 71

Qy  139  VSPIGNSSNNSSHWDLGSAFFFAGTVITTIGYGNIAPSTEGGKIFCILYAIFGIPLFGFL 198
         |:||| : |:|. ||:||||||||||||||||| ||:: |:: |:|:||
Db   72  VAITGNQTFN--NNWPNAMIFAATVITTIGYGNVAPKTPAGRIFCVFYGLFGVPL---C 126

Qy  199  LAGIGDQLGTIFGKSIARVEKVFRKKQVSQTKIRVISTILFILAGCIVFVTIPAVIFKYI 258
         | | |:|||| |  | . . |: :|:.|:| :| :|
Db  127  LTWI-SALGKFFGGRAKRLGQFLTKRGVSLRKAQITCTVIPIWVGVLVHLVIPPFVFMVT 185

Qy  259  EGWTALESIYFVVVTLTTVGFGDFVAGGNAGINYREWYKPLVWFWILVGLAYFAAVLSMI 318
         ||| | : : :|:.||:|:||||| |
Db  186  EGWNYIEGLYYSFITISTIGFGDFVAGVNPSANYHALYRYFVELWIYLGLA--------- 236

Qy  319  GDWLRLVLSKKTKEEVGEIKAHAAEWKANVTABFRETRRRLSVEIHDKLQRAATIRSMERR 378
         | | :: :: .: ||
Db  237  --WLSLF-----------------VNWKVS------MFVEVHKAIK----KRRRRR 263

Qy  379  RLGLDQRAHSLDMLSPEKRSVFAALDTGRFKASSQESINNRPNNLRLK----------GP 428
         : ||:||
Db  264  KESFESSPHSRKALQVKGSTASKDVNIFSFLSKKEETVNDLIKQIGKKAMKTSGGGETGP 323

Qy  429  -EQLNKHGQG---------------------------ASEDNIINKFGSTSRLTKRNKDLKKTLPED 468
         :: |
Db  324  GPGLGPQGGGLPALPPSLVPLVVYSKNRVPTLEEVSQTLRSKGHVSRSPDEEAVARAPED 383

Qy  469  VQKIYKTFRNYSLDEEKKEE-----------------TEKMCNSDNSSTAMLTDC 507
         ::
Db  384  SSPAPEVFMN-QLDRISEECEPWDAQDYHPLIFQDASIFVNTEAGLSDEETSKSSLEDN 442

Qy  508  I------QQHAE----LENGMIPTDTK 524
         :
Db  443  LAGEESPQQGAEAKAPLNMGEFPSSSE 469

RESULT 9
CIW1_HUMAN
ID   CIW1_HUMAN     STANDARD;      PRT;     336 AA.
AC   O00180; Q13307;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Potassium channel subfamily K member 1 (Inward rectifying potassium
DE   channel protein TWIK-1) (Potassium channel KCN01).
GN   KCNK1 OR TWIK OR HOHO1 OR KCNO1.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A., FUNCTION, AND MUTAGENESIS OF THR-161.
RC   TISSUE=Kidney;
RX   MEDLINE=96183184; PubMed=8605869;
RA   Lesage F., Guillemare E., Fink M., Duprat F., Lazdunski M., Romey G.,
RA   Barhanin J.;
RT   "TWIK-1, a ubiquitous human weakly inward rectifying K+ channel with a
RT   novel structure.";
RL   EMBO J. 15:1004-1011(1996).
RN   [2]
RP   SEQUENCE FROM N.A., AND REVIEW.
RC   TISSUE=Brain;
RX   MEDLINE=98122696; PubMed=9462864;
RA   Goldstein S.A.N., Wang K.-W., Ilan N., Pausch M.H.;
RT   "Sequence and function of the two P domain potassium channels:
RT   implications of an emerging superfamily.";
RL   J. Mol. Med. 76:13-20(1998).
RN   [3]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98026667; PubMed=9362344;
RA   Orias M., Velazquez H., Tung F., Lee G., Desir G.V.;
RT   "Cloning and localization of a double-pore K channel, KCNK1: exclusive
RT   expression in distal nephron segments.";
RL   Am. J. Physiol. 273:F663-F666(1997).
RN   [4]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length
RT   human and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC   -!- FUNCTION: Weakly inward rectifying potassium channel.
CC   -!- SUBUNIT: Homodimer (Potential).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC   -!- TISSUE SPECIFICITY: Widely expressed with high levels in heart and
CC       brain and lower levels in placenta, lung, liver and kidney.
CC   -!- MISCELLANEOUS: Inhibited by barium, quinidine, quinine and
CC       internal acidification. Activated by protein kinase C.
CC   -!- SIMILARITY: Belongs to the two pore domain potassium channel
CC       family.
CC   --------------------------------------------------------------------------
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CC   --------------------------------------------------------------------------
DR   EMBL; U33632; AAB01688.1; -.
DR   EMBL; U76996; AAB97878.1; -.
DR   EMBL; U90065; AAB51147.1; -.
DR   EMBL; BC018051; AAH18051.1; -.
DR   PIR; S65566; S65566.
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DR   Genew; HGNC:6272; KCNK1.
DR   MIM; 601745; -.
DR   GO; GO:0008076; C:voltage-gated potassium channel complex; TAS.
DR   GO; GO:0005242; F:inward rectifier potassium channel activity; TAS.
DR   GO; GO:0006813; P:potassium ion transport; TAS.
DR   InterPro; IPR003280; K+channel_2pore.
DR   InterPro; IPR001622; K+channel_pore.
DR   InterPro; IPR001779; TWIK1_channel.
DR   InterPro; IPR005408; TWIK_channel.
DR   PRINTS; PR01333; 2POREKCHANNEL.
DR   PRINTS; PR01096; TWIK1CHANNEL.
DR   PRINTS; PR01586; TWIKCHANNEL.
KW   Transport; Ion transport; Ionic channel; Voltage-gated channel;
KW   Potassium channel; Potassium; Transmembrane; Glycoprotein.
FT   DOMAIN         1     20       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM      21     41       POTENTIAL.
FT   DOMAIN       104    130       PORE-FORMING 1 (POTENTIAL).
FT   TRANSMEM     133    153       POTENTIAL.
FT   DOMAIN       154    177       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     178    198       POTENTIAL.
FT   DOMAIN       212    238       PORE-FORMING 2 (POTENTIAL).
FT   TRANSMEM     247    267       POTENTIAL.
FT   DOMAIN       268    336       CYTOPLASMIC (POTENTIAL).
FT   CARBOHYD      95     95       N-LINKED (GLCNAC...) (POTENTIAL).
FT   MUTAGEN      161    161       T->A: NO EFFECT ON CHANNEL ACTIVITY.
SQ   SEQUENCE   336 AA;  38143 MW;  2A41D9501323215D CRC64;

Query Match             14.6%;  Score 403;  DB 1;  Length 336;
Best Local Similarity   33.2%;  Pred. No. 9.6e-18;
  Matches   95;  Conservative   53;  Mismatches 104;  Indels  34;  Gaps   9;

Qy      76  FVVV--VVYLVTGGLVFRALEQPPESSQKNTIALEKAEFLRDHVCVSPQELETLIQHALD 133
                ||  : ::||| ||  :|| |||| :||:|| |: ::||:|||  :|: :|: |
Db      25  FLVLGYLILYLJVFGAVVFSSVELPYEDLLRQELRKLKRRFLEEHECLSEQLEQFLGRVLE  84

Qy     134  ADNAGVSPIGNSSNNSSHWDLGSAFFFAGTVITTIGYGNIAPSTEGGKIFCILYAIFGIP 193
                |||  |  | : | |   :|  |||||||::|| :||| ||:|||:| | :|| |||
Db      85  ASNYGVSVLSNASGN-WNWDFTSALFFASTVLSTTGYGHTVPLSDGGKAFCIIYSVIGIP 143

Qy     194  LFGPLLAGIGDQLGTIFGKSIARVEKVFRKKQV--------SQTKIRVISTIL--FILA 242
                |: |: :|: ||:|:  ::|  |::   :             :|: ::||   |:
Db     144  FTLLFLTAV-----------VQRITVHVTRRPVLYFHIRWGFSKQVVAIVHAVLLGFVTV 192

Qy     243  GCIVFVTIPAVIFKYIE-GWTALESIYFVVVTLLTTVGFGDFVAGGNAGINYREWYKPLVW 301
                || |||  || ||  | ||| | :|::|||||||||| |||| |:||:||  |:|:  |
Db     193  SCFFF--IPAAVFSVLEDDWNFLESFYFCFISLSTIGLGDYVPGEGYNQKFRELYKIGIT 250

Qy     302  FWILVGLAYPAAVLSMIGDWLRVLSK-----KTKEEVGEIKAHAAE 342
                ::|:|| |:|  :|: || :|| |:|         |: :: :| :
Db     251  CYILLGLIAMLVVLETFCE-LHELKKFRKMFYVKKDKDEDQVHIIE 295
```

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CIWH_HUMAN
ID   CIWH_HUMAN     STANDARD;     PRT;    332 AA.
AC   Q96T54; Q8TAW4; Q9BXD1; Q9H592;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Potassium channel subfamily K member 17 (TWIK-related alkaline pH
DE   activated K+ channel 2) (2P domain potassium channel Talk-2) (TWIK-
DE   related acid-sensitive K+ channel 4) (TASK-4).
GN   KCNK17 OR TALK2 OR TASK4.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORM 1).
RC   TISSUE=Pancreas;
RX   MEDLINE=21164727; PubMed=11263999;
RA   Girard C., Duprat F., Terrenoire C., Tinel N., Fosset M., Romey G.,
RA   Lazdunski M., Lesage F.;
```

```
RT   "Genomic and functional characteristics of novel human pancreatic 2P
RT   domain K(+) channels.";
RL   Biochem. Biophys. Res. Commun. 282:249-256 (2001).
RN   [2]
RP   SEQUENCE FROM N.A. (ISOFORM 2).
RC   TISSUE=Adrenal gland;
RX   MEDLINE=21145510; PubMed=11248242;
RA   Decher N., Maier M., Dittrich W., Gassenhuber J., Brueggemann A.,
RA   Busch A.E., Steinmeyer K.;
RT   "Characterization of TASK-4, a novel member of the pH-sensitive,
RT   two-pore domain potassium channel family.";
RL   FEBS Lett. 492:84-89(2001).
RN   [3]
RP   SEQUENCE FROM N.A. (ISOFORM 1).
RA   Williams S.;
RL   Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   SEQUENCE FROM N.A. (ISOFORM 1).
RC   TISSUE=Lung, and Spleen;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length
RT   human and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC   -!- FUNCTION: Outward rectifying potassium channel. Produces rapidly
CC       activating and non-inactivating outward rectifier K(+) currents.
CC   -!- SUBUNIT: Homodimer (Potential).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC       Name=1;
CC         IsoId=Q96T54-1; Sequence=Displayed;
CC       Name=2;
CC         IsoId=Q96T54-2; Sequence=VSP_006700;
CC         Note=No experimental confirmation available;
CC   -!- MISCELLANEOUS: inhibited by Ba(+2), quinidine, chloroform and
CC       halothane. Activated at alkaline pH. Activated by quinine and
CC       isoflurane.
CC   -!- SIMILARITY: Belongs to the two pore domain potassium channel
CC       family.
CC   -!- CAUTION: Ref.3 sequence differs from that shown due to erroneous
CC       gene model prediction.
CC   -----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   -----------------------------------------------------------------------
DR   EMBL; AF358910; AAK49533.1; -.
DR   EMBL; AF333912; AAK28551.1; -.
DR   EMBL; AL136087; CAC07335.1; ALT_SEQ.
DR   EMBL; BC025726; AAH25726.1; -.
DR   Genew; HGNC:14465; KCNK17.
DR   MIM; 607370; -.
DR   InterPro; IPR003280; K+channel_2pore.
DR   InterPro; IPR001622; K+channel_pore.
DR   InterPro; IPR003092; TASK_channel.
DR   PRINTS; PR01333; 2POREKCHANNEL.
DR   PRINTS; PR01095; TASKCHANNEL.
KW   Transport; Ion transport; Ionic channel; Voltage-gated channel;
KW   Potassium channel; Potassium; Transmembrane; Glycoprotein;
KW   Alternative splicing.
FT   DOMAIN        1     20       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     21     43       POTENTIAL.
FT   DOMAIN      106    124       PORE-FORMING 1 (POTENTIAL).
FT   TRANSMEM    128    148       POTENTIAL.
FT   DOMAIN      149    179       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    180    200       POTENTIAL.
FT   DOMAIN      211    230       PORE-FORMING 2 (POTENTIAL).
FT   TRANSMEM    244    264       POTENTIAL.
FT   DOMAIN      265    332       CYTOPLASMIC (POTENTIAL).
FT   CARBOHYD     65     65       N-LINKED (GLCNAC....) (POTENTIAL).
FT   CARBOHYD     94     94       N-LINKED (GLCNAC....) (POTENTIAL).
FT   VARSPLIC    260    332       IKLILSQLETPGRVCSCCHHSSKEDFKSQSWRQGPDREPES
FT                                HSFQQGCYPEGPMGIIQHLEPSAHAAGCGKDS -> SNSSS
FT                                PSWRRQGGVPAATTALRKTSSPKAGDRDLTGSGSPTPHSK
FT                                DAIQRDPWSYSIWNLLLTLQAVARTASYTPFFGRRPR
FT                                (in isoform 2)
FT                                /FTId=VSP_006700.
FT   CONFLICT     21     21       S -> G (IN REF. 2 AND 4).
SQ   SEQUENCE   332 AA;  36894 MW;  1848DBC06E078158 CRC64;

Query Match             14.2%;  Score 392;  DB 1;  Length 332;
Best Local Similarity   31.2%;  Pred. No. 4.4e-17;
Matches   85;  Conservative   59;  Mismatches  114;  Indels  14;  Gaps   3;

Qy       47 SRATVVARMEGTSQGGLQTVMKWKITVVAIFVVVVYLVTGGLVFRALEQPFESSQKNTIA 106
                ||:  :|               :|:|      ||||
Db        6 ARAAPEGRVRGCAV-------PSTVLLLAYLAYLALGTGVFWTLEGRAAQDSRSFQ 56

Qy      107 LEKAEFLRDHVCVSPQELETLIQHALDADNAGVSPIGNSSNNSSHWDLGSAFFFAGTVIT 166
                |||:|| :||:| | ||||  :||| :|:: |||:: | ||| |   ||:|||
Db       57 RDKWELLQNFTCLDRPALDSLIRDVVQAYKNGASLLSNTT-SMGRWELVGSFFFSVSTIT 115

Qy      167 TIGYGNIAPSTEGGKIFCILYAIFGIPLFGFLLAGIGDQLGTIFGKSIARVEKVFRKKQV 226
            ||||||:::|:| ||||| ||||| :||||  :|   |  |:||||||       :||||
Db      116 TIGYGNLSPNTMAARLFCIFFALVGIPLNLVL---NRLGHLMQQGVNHWASRLGGTWQ 171

Qy      227 SQTKIRVISTILFILAGCIVFVTIPAVIFKYIEGWTALESSIYFVVVTLTTVGFGDFVAGG 286
            |||:||| ||| ||||  |:||:||| ||   :|||  :| |:  ||:||::||:||:|
Db      172 DPDKARWLAGSGALLSGLLFLLLPLLFSHMEGWSYTEGFYFAFITLSTVGFGDYVIGM 231

Qy      287 NAGINYREWYKPLVWFWILVGLAYFAAVLSMI 318
            ||||||||||||:||:|| :| ||:  ::: :|
Db      232 NPSQRYPLWYKNMVSLWILFGMAWLALIIKLI 263
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RESULT 11
CIW1_MOUSE
ID   CIW1_MOUSE               STANDARD;      PRT;   336 AA.
AC   O08581;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Potassium channel subfamily K member 1 (Inward rectifying potassium
DE   channel protein TWIK-1).
GN   KCNK1.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=97165959; PubMed=9013852;
RA   Lesage F., Lauritzen I., Duprat F., Reyes R., Fink M., Heurteaux C.,
RA   Lazdunski M.;
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Qy  194  LFGFLLAGIGDQLGTIFGKSIARVEKVFRKKQV----------SQTKIRVISTIL--FILA 242
                                            : :|.        ||.| | .|::| ||.|
Db  144  FTLLFLTAL---------VQRVTVHVTRRPVLYFHIRWGFSKQVVAIVHAVLLGFVTV 192

Qy  243  GCIVFVTIPAVIFKYIE-GWTALESIYFVVVTLTTVGFGDFVAGNAGINYREWYKPLVW 301
               |:|  || | |:   | : .  | :||| |: ::|  |||:| | ||.|  :|
Db  193  SCFFF-----IPAAVFSVLEDDWNFLESFYFCFISLSTIGLGDYVPGEGYNQKFRELYKIGIT 250

Qy  302  FWILVGLAYFPAAVLSMIGDWLRVLS--------KKTKEE 332
            |:  :|||     |   |        || |:|
Db  251  CYLLLGLITMLVVLETFCE-LHELKKFRKMFYVKDXDE 288
```

```
RT   "The structure, function and distribution of the mouse TWIK-1 K+
RT   channel.";
RL   FEBS Lett. 402:28-32(1997).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=129/SvJ; TISSUE=Liver;
RX   MEDLINE=98218573; PubMed=9559671;
RA   Arrighi I., Lesage F., Scineca J.-C., Carle G.F., Barhanin J.;
RT   "Structure, chromosome localization, and tissue distribution of the
RT   mouse twik K+ channel gene.";
RL   FEBS Lett. 425:310-316(1998).
CC   -!- FUNCTION: Weak inwardly rectifying potassium channel.
CC   -!- SUBUNIT: Homodimer (Potential).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC   -!- TISSUE SPECIFICITY: Widely expressed. Highest expression in brain,
CC       kidney, thyroid, salivary gland, adrenal gland, prostate,
CC       epididymis, uterus, placenta, colon and jejunum. Moderate
CC       expression in eyes, pituitary, pancreas, smooth muscle, testis and
CC       ovary. Very low levels in lung, aorta, liver, heart, skeletal
CC       muscle, thymus and spleen. In the brain, highest expression in
CC       cerebellar granule cells, brainstem, hippocampus and cerebral
CC       cortex.
CC   -!- DEVELOPMENTAL STAGE: EXPRESSION DETECTED AS EARLY AS 7 DAYS POST
CC       CONCEPTION. EXPRESSION INCREASES FROM 2-8 DAYS AFTER BIRTH AND
CC       STABILIZES AFTER DAY 8.
CC   -!- MISCELLANEOUS: INHIBITED BY QUININE, BARIUM, AND INTERNAL
CC       ACIDIFICATION. ACTIVATED BY PROTEIN KINASE C.
CC   -!- SIMILARITY: Belongs to the two pore domain potassium channel
CC       family.
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RESULT 12
CIW3_MOUSE
ID   CIW3_MOUSE     STANDARD;      PRT;    409 AA.
AC   O35111; O35163;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Potassium channel subfamily K member 3 (Acid-sensitive potassium
DE   channel protein TASK-1) (TWIK-related acid-sensitive K+ channel 1)
DE   (Cardiac two-pore background K+ channel) (cTBAK-1) (Two pore potassium
DE   channel KT3.1).
GN   KCNK3 OR TASK1 OR TASK OR CTBAK.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Heart;
RX   MEDLINE=98165556; PubMed=9506712;
RA   Kim D., Fujita A., Horio Y., Kurachi Y.;
RT   "Cloning and functional expression of a novel cardiac two-pore
RT   background K+ channel (cTBAK-1).";
RL   Circ. Res. 82:513-518(1998).
RN   [2]
RP   SEQUENCE OF 4-409 FROM N.A.
RC   TISSUE=Heart;
RX   MEDLINE=20287574; PubMed=10748056;
RA   Lopes C.M., Gallagher P.G., Buck M.E., Butler M.H., Goldstein S.A.;
RT   "Proton block and voltage gating are potassium-dependent in the
RT   cardiac leak channel Kcnk3.";
RL   J. Biol. Chem. 275:16969-16978(2000).
RN   [3]
RP   SEQUENCE OF 4-409 FROM N.A.
RX   MEDLINE=97459932; PubMed=9312005;
RA   Duprat F., Lesage F., Fink M., Reyes R., Heurteaux C., Lazdunski M.;
RT   "TASK, a human background K+ channel to sense external pH variations
RT   near physiological pH.";
RL   EMBO J. 16:5464-5471(1997).
CC   -!- FUNCTION: PH-DEPENDENT, VOLTAGE-INSENSITIVE, BACKGROUND POTASSIUM
CC       CHANNEL PROTEIN. RECTIFICATION DIRECTION RESULTS FROM POTASSIUM
CC       ION CONCENTRATION ON EITHER SIDE OF THE MEMBRANE. ACTS AS AN
CC       OUTWARD RECTIFIER WHEN EXTERNAL POTASSIUM CONCENTRATION IS LOW.
CC       WHEN EXTERNAL POTASSIUM CONCENTRATION IS HIGH, CURRENT IS INWARD
CC       (BY SIMILARITY).
CC   -!- SUBUNIT: Homodimer (Potential).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC   -!- TISSUE SPECIFICITY: VERY STRONG EXPRESSION IN HEART, ALSO DETECTED
CC       IN KIDNEY, BRAIN, SKIN, TESTIS, LUNG, SKELETAL MUSCLE, SMALL
CC       INTESTINE AND STOMACH. NOT DETECTED IN LIVER, THYMUS OR SPLEEN.
CC   -!- MISCELLANEOUS: INACTIVATED BY BARIUM.
CC   -!- SIMILARITY: Belongs to the two pore domain potassium channel
CC       family.
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DR   EMBL; AF033017; AAC16973.1; -.
DR   MGD; MGI:1103322; Kcnk1.
DR   InterPro; IPR003280; K+channel_2pore.
DR   InterPro; IPR001622; K+channel_pore.
DR   InterPro; IPR001779; TWIK_channel.
DR   InterPro; IPR005408; TWIK_channel.
DR   PRINTS; PR01333; 2POREKCHANNEL.
DR   PRINTS; PR01096; TWIKICHANNEL.
DR   PRINTS; PR01586; TWIKICHANNEL.
KW   Transport; Ion transport; Ionic channel; Voltage-gated channel;
KW   Potassium channel; Potassium; Transmembrane; Glycoprotein.
FT   DOMAIN        1     20   CYTOPLASMIC (POTENTIAL).
FT   DOMAIN       21     41   POTENTIAL.
FT   TRANSMEM     21     41   POTENTIAL.
FT   DOMAIN      104    130   PORE-FORMING 1 (POTENTIAL).
FT   TRANSMEM    133    153   POTENTIAL.
FT   DOMAIN      154    177   CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    178    198   POTENTIAL.
FT   DOMAIN      212    238   PORE-FORMING 2 (POTENTIAL).
FT   TRANSMEM    247    267   POTENTIAL.
FT   DOMAIN      268    336   CYTOPLASMIC (POTENTIAL).
FT   CARBOHYD     95     95   N-LINKED (GLCNAC...) (POTENTIAL).
SQ   SEQUENCE   336 AA;   38275 MW;   A996060A18266FD4 CRC64;
```

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Query Match             14.1%;
Best Local Similarity   33.7%;    Pred. No. 5.6e-17;
Matches  94;  Conservative  49;  Mismatches  99;  Indels  37;  Gaps  9;
Score 390.5; DB 1; Length 336;

Qy   76  FVVV--VVYLVTGGLVFRALEQPFESSQXNTIALEKAEFLRDHVCVSPQELETLIQHALD 133
             :. ::||| :|| |.|:  || |: :|  ||..|  |::|  ||: |:|:|| :|
Db   25  FIVLGYILYLLVFGAVVFSSEELPYEDLLRQELRKLKRRFLEEHECLSEPQLEQFLGRVLE 84

Qy  134  ADNAGVSPIGNSSNNGSSHWDLGSAFFFAGTVITTIGYGNIAPSTEGGKIFCILYAIFGIP 193
             ::|||:|: :.|:.|. |:.  | | .|:| |:||:||.  :|:.||| ||::|::.|||
Db   85  ASNYGVSVLSNASGN-WNWDFTSALFFASTVLSTTGYGHTVPLSDGGKAFCIIYSVIGIP 143
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OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Cerebellum;
RX   MEDLINE=98099797; PubMed=9437008;
RA   Leonoudakis D., Gray A.T., Winegar B.D., Kindler C.H., Harada M.,
RA   Taylor D.M., Chavez R.A., Forsayeth J.R., Yost C.S.;
RT   "An open rectifier potassium channel with two pore domains in tandem
RT   cloned from rat cerebellum.";
RL   J. Neurosci. 18:868-877(1998).
CC   -!- FUNCTION: PH-DEPENDENT, VOLTAGE-INSENSITIVE, BACKGROUND POTASSIUM
CC       CHANNEL PROTEIN. RECTIFICATION DIRECTION RESULTS FROM POTASSIUM
CC       ION CONCENTRATION ON EITHER SIDE OF THE MEMBRANE. ACTS AS AN
CC       OUTWARD RECTIFIER WHEN EXTERNAL POTASSIUM CONCENTRATION IS LOW.
CC       WHEN EXTERNAL POTASSIUM CONCENTRATION IS HIGH, CURRENT IS INWARD
CC       (BY SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC   -!- TISSUE SPECIFICITY: STRONGEST EXPRESSION IN HEART. MODERATE
CC       EXPRESSION IN LUNG AND BRAIN. LOW LEVELS IN LIVER, KIDNEY AND
CC       SKELETAL MUSCLE.
CC   -!- MISCELLANEOUS: INHIBITED BY EXTRACELLULAR ACIDIFICATION, ZINC,
CC       BUPIVACAINE AND PHENYTOIN. ACTIVATED BY PROTEIN KINASE A.
CC   -!- SIMILARITY: Belongs to the two pore domain potassium channel
CC       family.
CC   --------------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
DR   EMBL; AF031384; AAC39952.1; -.
DR   InterPro; IPR005821; Ion_trans.
DR   InterPro; IPR003280; K+channel_2pore.
DR   InterPro; IPR001622; K+channel_pore.
DR   InterPro; IPR005406; TASK1_channel.
DR   InterPro; IPR003092; TASK_channel.
DR   Pfam; PF00520; ion_trans; 1.
DR   PRINTS; PR01333; 2POREKCHANNEL.
DR   PRINTS; PR01584; TASK1CHANNEL.
DR   PRINTS; PR01095; TASKCHANNEL.
KW   Transport; Ion transport; Ionic channel; Voltage-gated channel;
KW   Potassium channel; Potassium; Transmembrane; Glycoprotein.
FT   DOMAIN        1      8       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM      9     29       POTENTIAL.
FT   DOMAIN       78    101       PORE-FORMING 1 (POTENTIAL).
FT   TRANSMEM    108    128       POTENTIAL.
FT   DOMAIN      129    158       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    159    179       POTENTIAL.
FT   DOMAIN      184    207       PORE-FORMING 2 (POTENTIAL).
FT   TRANSMEM    223    243       POTENTIAL.
FT   DOMAIN      244    411       CYTOPLASMIC (POTENTIAL).
FT   CARBOHYD     53     53       N-LINKED (GLCNAC...) (POTENTIAL).
SQ   SEQUENCE   411 AA;  45276 MW;  D2778016E09S2BF5 CRC64;

Query Match             12.8%;  Score 352.5;  DB 1;  Length 411;
Best Local Similarity   32.3%;  Pred. No. 1.5e-14;
Matches   93;  Conservative   54;  Mismatches  112;  Indels   29;  Gaps    9;

Qy     67 MKWKTV--VAIFVVVVVYLVTGGLVFRALEQPFESSQKNTIALEKAEFLRDHVCVSP--- 121
          |||:||||  :|:|||:|  |||||:::|: |:           ::||
Db      1 MKRQNVRTLALIVCTFTYLLVGAAVFDALESEPEMIERQRLELRQLE-LRARYNLSEGGY 59

Qy    122 QELETLIQHALDADNAGVSPIGNSSNNSSHWDLGSAFFFAGTVITTIGYGNIAPSTEGGK 181
          :||||:||          |||                  ::|:|||||||||:||||:|||
Db     60 EELERVVLR-LKPHKAGV---------QWRFAGSFYFAITVITTIGYGHAAPSTDGGK 107

Qy    182 IFCILYAIFGIPLFGFLLAGIGDQLGTIFGKSIARVEKVFRKKQVSQTKIRVISTILFIL 241
          :||: ||:|  ||||| :  |::||:|  |   | :::||::
Db    108 VFCMFYALLGIPLTLVMFQSLGERINTFVRYLLHRAK--RGLGMRHAEVSMANMVLIGF 164
```

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CC   or send an email to license@isb-sib.ch).
CC
DR   EMBL; AB008537; BAA25436.1; -.
DR   EMBL; AF241798; AAF81418.1; -.
DR   EMBL; AF242508; AAF81418.1; JOINED.
DR   EMBL; AF065162; AAG29339.1; -.
DR   EMBL; AF006824; AAC53367.1; -.
DR   EMBL; AB013345; BAA28349.1; -.
DR   MGD; MGI:1100509; Kcnk3.
DR   InterPro; IPR005821; Ion_trans.
DR   InterPro; IPR003280; K+channel_2pore.
DR   InterPro; IPR001622; K+channel_pore.
DR   InterPro; IPR005406; TASK1_channel.
DR   InterPro; IPR003092; TASK_channel.
DR   Pfam; PF00520; ion_trans;1.
DR   PRINTS; PR01333; 2POREKCHANNEL.
DR   PRINTS; PR01584; TASK1CHANNEL.
DR   PRINTS; PR01095; TASKCHANNEL.
KW   Transport; Ion transport; Ionic channel; Voltage-gated channel;
KW   Potassium channel; Potassium; Transmembrane; Glycoprotein.
FT   DOMAIN        1      8       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM      9     29       POTENTIAL.
FT   DOMAIN       78    101       PORE-FORMING 1 (POTENTIAL).
FT   TRANSMEM    108    128       POTENTIAL.
FT   DOMAIN      129    158       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    159    179       POTENTIAL.
FT   DOMAIN      184    207       PORE-FORMING 2 (POTENTIAL).
FT   TRANSMEM    223    243       POTENTIAL.
FT   DOMAIN      244    409       CYTOPLASMIC (POTENTIAL).
FT   CARBOHYD     53     53       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CONFLICT      4      4       Q -> E (IN REF. 3).
FT   CONFLICT    123    123       V -> I (IN REF. 3).
SQ   SEQUENCE   409 AA;  45068 MW;  35236E011AAC5687 CRC64;

Query Match             12.8%;  Score 352.5;  DB 1;  Length 409;
Best Local Similarity   32.3%;  Pred. No. 1.5e-14;
Matches   93;  Conservative   54;  Mismatches  112;  Indels   29;  Gaps    9;

Qy     67 MKWKTV--VAIFVVVVVYLVTGGLVFRALEQPFESSQKNTIALEKAEFLRDHVCVSP--- 121
          |||:||||  :|:|||:|  |||||:::|: |:           ::||
Db      1 MKRQNVRTLALIVCTFTYLLVGAAVFDALESEPEMIERQRLELRQLE-LRARYNLSEGGY 59

Qy    122 QELETLIQHALDADNAGVSPIGNSSNNSSHWDLGSAFFFAGTVITTIGYGNIAPSTEGGK 181
          :||||:||          |||                  ::|:|||||||||:||||:|||
Db     60 EELERVVLR-LKPHKAGV---------QWRFAGSFYFAITVITTIGYGHAAPSTDGGK 107

Qy    182 IFCILYAIFGIPLFGFLLAGIGDQLGTIFGKSIARVEKVFRKKQVSQTKIRVISTILFIL 241
          :||: ||:|  ||||| :  |::||:|  |   | :::||::
Db    108 VFCMFYALLGIPLTLVMFQSLGERINTFVRYLLHRAK--RGLGMRHAEVSMANMVLIGF 164

Qy    242 AGIVFVTIPAVIFKIEGWTALESIYFVVVTLITVGFGDFVA-GGNAGINYREWYKPLV 300
                                                 ||
Db    165 VSCISTLCIGAAAFSYYERWTFFQAYYYCFITLTTIGFGDYVALQKDQALQTPQYVAFS 224

Qy    301 WFWILVGLAYFAAVLSMIGDWLRVLSKKTKEVGEIKAHAAEWKANVT 348
          :  :|||:: ||:||    |:  :  ||:   :::|
Db    225 FVYIILTGLTVIGAFLNIV--VLRFMTMNAEDEKRD-----AEHRALLT 265


RESULT 13
CIW3_RAT
ID   CIW3_RAT     STANDARD;      PRT;   411 AA.
AC   O54912;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Potassium channel subfamily K member 3 (Acid-sensitive potassium
DE   channel protein TASK-1) (TWIK-related acid-sensitive K+ channel 1)
DE   (Two pore potassium channel KT3.1).
GN   KCNK3 OR TASK1 OR TASK.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
```

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Qy   67 MKWKTV--VAIFVVVVVLVTGGLVFRALEQPFSSQKNTIALEKAEFLRDHVCVSPQ--  122
           ||:|  ||::||   :|||:|||||| ||:|     || :   || |||||| |
Db    1 MKKQNVRTLSLIACTFTYLLVGAAVFDALESDHEMREEKLKAEEIR-IRGKYNISTEDY  59

Qy  123 -ELETLIQHALDADNAGVSPIGNSNNSSHWDLGSAFFPAGTVITTIGVGNIAPSTEGGK 181
          :||:|:|            ||||||              |||||||||||||||||||
Db   60 RQLELVILQS-EPHRAGV-------------------QWKFAGSFYFAITVITTIGYGHAAPGTDAGK 107

Qy  182 IFCILYAIFGIPLFGFLLAGIGDQLGTIFGKSIARVEKV--FRKKQVSQTKIRVISTILF 239
          ::  ||| :  |:|||   :|||:  |:|  |:||||||:     ::::||  ||:
Db  108 AFCMFYAVLGIPLTLVMFQSLGERMNTFVRYLLKIKKCCGMRNTEVSMENMVTVG----  163

Qy  240 ILAGCIVFVTIPAVIFKYIEGWTALESIYFVVVTLTTVGFGDFVAGGNAG-INYREWYKP 298
          || |||||||||||||||||||||||||||||||||||||||||         ||||||
Db  164 -FFSCMGTLCIGAAAFSQCEEWSFFHAYYYCFITLTTIGFGDYVALQSKGALQRKPFVVA 222

Qy  299 LVWFWILVGLAYFPAAVLSMIGDWLRVLSKKTKEEVGE------IKAHAAEWKANVTAEFR 352
          |:  ||||:||||:||:| ||||:|||:||||:||||:        ||:
Db  223 FSFMYILVGLTVIGAFLNLV--VLRFLTWNSDERGEGEGAALFGNPSSVVTHISEEAR  280

Qy  353 ETRRRLSVEIHD--KLQRAATIRSMERRRIG---LDQRAHS----LDMLSPE--KRSVFA 401
          ::   ||:|  :   |: |||     :||:|         :        ||     :|
Db  281 QVRQRYRGEGGDLQSVCSCACYRS-QPQNFGATLAPQPLHSISCRIEEISPSTLKNSLF-  338

Qy  402 ALDTGRFKASSQESINRPNNLRLKGPEQLNKHGQGASEDNIINKFGSTSRLTKRK 457
          :|                                        :: :
Db  339 -----------------------------PSPISSVSPG-----LHSFGDNHRLMLRR 362
```

RESULT 14

```
CIW9_CAVPO
ID   CIW9_CAVPO     STANDARD;      PRT;    365 AA.
AC   Q9JL58;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Potassium channel subfamily K member 9 (Acid-sensitive potassium
DE   channel protein TASK-3) (TWIK-related acid-sensitive K+ channel 3).
GN   KCNK9 OR TASK3.
OS   Cavia porcellus (Guinea pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX   NCBI_TaxID=10141;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=20287530; PubMed=10747866;
RA   Rajan S., Wischmeyer E., Liu G.X., Preisig-Mueller R., Daut J.,
RA   Karschin A., Derst C.;
RT   "TASK-3, a novel tandem pore domain acid-sensitive K+ channel. An
RT   extracellular histidine as pH sensor.";
RL   J. Biol. Chem. 275:16650-16657(2000).
CC   -!- FUNCTION: pH-dependent, voltage-insensitive, background potassium
CC       channel protein.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC   -!- SIMILARITY: Belongs to the two pore domain potassium channel
CC       family.
CC   --------------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; AF212827; AAF63706.1; -.
DR   InterPro; IPR005821; Ion_trans.
DR   InterPro; IPR003280; K+channel_2pore.
DR   InterPro; IPR001622; K+channel_pore.
DR   InterPro; IPR005407; TASK3_channel.
DR   InterPro; IPR003092; TASK_channel.
DR   Pfam; PF00520; ion_trans;_1.
DR   PRINTS; PR01333; 2POREKCHANNEL.
DR   PRINTS; PR01585; TASK3CHANNEL.
DR   PRINTS; PR01095; TASKCHANNEL.
KW   Transport; Ion transport; Ionic channel; Voltage-gated channel;
KW   Potassium channel; Potassium; Transmembrane; Glycoprotein.
FT   DOMAIN        1      8       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM      9     29       POTENTIAL.
FT   DOMAIN       30    101       PORE-FORMING 1 (POTENTIAL).
FT   TRANSMEM    108    128       POTENTIAL.
FT   DOMAIN      129    158       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    159    179       POTENTIAL.
FT   DOMAIN      184    207       PORE-FORMING 2 (POTENTIAL).
FT   TRANSMEM    219    239       POTENTIAL.
FT   DOMAIN      240    365       CYTOPLASMIC (POTENTIAL).
FT   CARBOHYD     53     53       N-LINKED (GLCNAC....) (POTENTIAL).
SQ   SEQUENCE   365 AA;  40769 MW;  261DC973FF53AF91 CRC64;
```

```
Qy  242 AGCIVFVTIPAVIFKYIEGWTALESIYFVVVTLTTVGFGDFVA-GGNAGINYREWYKPLV 300
          ||:|||||||||||||||||||||   |||||:||||||||||   ||: |   || |:
Db  165 VSCISTLCIGAAAFSYERWTFFQAYYYCFITLTTIGFGDVALQKDQALQTQPQVVAFS 224

Qy  301 WFWILVGLAYFPAAVLSMIGDWLRVLSKKTKEEVGEIKAHAAEWKANVT 348
          :|||||||| |   || |||||||:   ||::| |||||||||
Db  225 FVYILTGLTVIGAFLNLV--VLRFMTWNAEDEKRD----AEHRALLT 265
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RESULT 15

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CIW3_HUMAN
ID   CIW3_HUMAN     STANDARD;      PRT;    394 AA.
AC   O14649;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Potassium channel subfamily K member 3 (Acid-sensitive potassium
DE   channel protein TASK-1) (TWIK-related acid-sensitive K+ channel 1)
DE   (Two pore potassium channel KT3.1).
GN   KCNK3 OR TASK1 OR TASK.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Kidney;
RX   MEDLINE=97459932; PubMed=9312005;
RA   Duprat F., Lesage F., Fink M., Reyes R., Heurteaux C., Lazdunski M.;
RT   "TASK, a human background K+ channel to sense external pH variations
RT   near physiological pH.";
RL   EMBO J. 16:5464-5471(1997).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Heart;
RA   Lopes C.M.B., Gallagher P.G., Buck M.E., Butler M.H.,
RA   Goldstein S.A.N.;
RT   "Proton block and voltage-gating are potassium-dependent in the
RT   cardiac leak channel Kcnk3.";
RL   Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   ACTIVATION.
RX   MEDLINE=99254548; PubMed=10321245;
RA   Patel A.J., Honore E., Lesage F., Fink M., Romey G., Lazdunski M.;
RT   "Inhalational anesthetics activate two-pore-domain background K+
RT   channels.";
RL   Nat. Neurosci. 2:422-426(1999).
RN   [4]
RP   MUTAGENESIS OF HIS-98.
RX   MEDLINE=21535313; PubMed=11680614;
RA   Ashmole I., Goodwin P.A., Stanfield P.R.;
RT   "TASK-5, a novel member of the tandem pore K+ channel family.";
```

Query Match       12.7%;  Score 350.5; DB 1;  Length 365;
Best Local Similarity 26.9%;  Pred. No. 1.7e-14;
Matches  112;  Conservative  72;  Mismatches 153;  Indels  79;  Gaps  17;

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RL   Pflugers Arch. 442:828-833 (2001).
CC   -!- FUNCTION: PH-DEPENDENT, VOLTAGE-INSENSITIVE, BACKGROUND POTASSIUM
CC       CHANNEL PROTEIN. RECTIFICATION DIRECTION RESULTS FROM POTASSIUM
CC       ION CONCENTRATION ON EITHER SIDE OF THE MEMBRANE. ACTS AS AN
CC       OUTWARD RECTIFIER WHEN EXTERNAL POTASSIUM CONCENTRATION IS LOW.
CC       WHEN EXTERNAL POTASSIUM CONCENTRATION IS HIGH, CURRENT IS INWARD.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC   -!- TISSUE SPECIFICITY: WIDESPREAD EXPRESSION IN ADULT. STRONGEST
CC       EXPRESSION IN PANCREAS AND PLACENTA. LOWER EXPRESSION IN BRAIN,
CC       LUNG, PROSTATE, HEART, KIDNEY, UTERUS, SMALL INTESTINE AND COLON.
CC   -!- MISCELLANEOUS: INHIBITED BY EXTERNAL ACIDIFICATION. ACTIVATED BY
CC       HALOTHANE AND ISOFLURANE.
CC   -!- SIMILARITY: Belongs to the two pore domain potassium channel
CC       family.
CC   ------------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ------------------------------------------------------------------------
DR   EMBL; AF006823; AAC51777.1; -.
DR   EMBL; AF065163; AAG29340.1; -.
DR   Genew; HGNC:6278; KCNK3.
DR   MIM; 603220; -.
DR   GO; GO:0005887; C:integral to plasma membrane; TAS.
DR   GO; GO:0005267; F:potassium channel activity; TAS.
DR   GO; GO:0006813; P:potassium ion transport; TAS.
DR   GO; GO:0007268; P:synaptic transmission; TAS.
DR   InterPro; IPR005821; ion_trans.
DR   InterPro; IPR003280; K-channel_2pore.
DR   InterPro; IPR001622; K-channel_pore.
DR   InterPro; IPR005406; TASK1_channel.
DR   InterPro; IPR003092; TASK_channel.
DR   Pfam; PF00520; ion_trans; 1.
DR   PRINTS; PR01333; 2POREKCHANNEL.
DR   PRINTS; PR01584; TASK1CHANNEL.
DR   PRINTS; PR01095; TASKCHANNEL.
KW   Transport; Ion transport; Ionic channel; Voltage-gated channel;
KW   Potassium channel; Potassium; Transmembrane; Glycoprotein.
FT   DOMAIN        1      8       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM      9     29       POTENTIAL.
FT   DOMAIN       29     29       PORE-FORMING 1 (POTENTIAL).
FT   TRANSMEM     78    101       POTENTIAL.
FT   DOMAIN      108    128       POTENTIAL.
FT   DOMAIN      129    158       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    159    179       POTENTIAL.
FT   DOMAIN      184    207       PORE-FORMING 2 (POTENTIAL).
FT   TRANSMEM    223    243       POTENTIAL.
FT   DOMAIN      244    394       CYTOPLASMIC (POTENTIAL).
FT   CARBOHYD     53     53       N-LINKED (GLCNAC...) (POTENTIAL).
FT   MUTAGEN      98     98       H->N: GREATLY REDUCES PH SENSITIVITY.
SQ   SEQUENCE    394 AA;  43518 MW;  9FF4C8266F615FB7 CRC64;
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Query Match                 12.7%;  Score 349.5;  DB 1;  Length 394;
Best Local Similarity       32.8%;  Pred. No. 2.1e-14;
Matches    95;  Conservative 53;  Mismatches 109;  Indels 33;  Gaps 10;

Qy    67 MKWKITV--VAIFVVVVVIVTGGLVFRALEQPFESSQKNTIALEKAEFLRDHVCVSP--- 121
         :||:|| ::|  :|: |||:|:||:|| |||: ||:      :: :|: : :|:|
Db     1 MKRQNVRTLALIVCTFTYLLVGAAVFDALESEPELIERQRLELRQQE-LRARYNLSQGGY  59

Qy   122 QELETLIQHALDADNAGVSPIGNSSNNSSHWDLGSAFFAGTVITTIGYGNIAPSTEGGK  181
         :||:|: |||   ||        ||:|| |||||||:::|| ||||||||:|||||||
Db    60 EELERVVLR-LKPHKAGV---------QWRFAGSFYFAITVITTIGYGHAAPSTDGGK  107

Qy   182 IFCILYAIFGIPLFGPILAGIGDQLGTIFGKSIARVEK--VFRKKQVSQTKIRVISTILF 239
         |::||| |:|||||||||||:||:|||:||||||||    :|
Db   108 VFCMFYALLGIPLTLVMFQSLGERINTLVRYLLHRAKKGLGMRRADVSMANM----VLI 162

Qy   240 ILAGCVFVTIPAVIFKYIEGWTALESIYFVVTLTTVGFGDFVA-GGNAGINYREWYKP 298
         ||: || ||   :||:|:|  :|::|:: |:  :||:||||:|| | :  :  :
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```
Db   163 GFFSCISTLCIGAAAFSHYEHWTFFQAYYCPITLITIGFGDYVALQKDQALQTQPQYVA 222

Qy   299 LVWFWILVGLAYFAAVLSMIGDWLRVLSKKTKEEVGEIKAHAAEWKANVT 348
         |::||: ::|:|:    ::|:      ::|  :: :  :: |:|
Db   223 FSFVYILTGLTVIGAFLNLV--VLRFMTMNAEDEKRD----AEHRALLT 265

Search completed: June 29, 2004, 18:18:24
Job time : 19 secs
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